

FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTGT
GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT
CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA
TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC
CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT
ACACGTGGAGTCCTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG
CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTG
CCCATATCTATTACCGTGTTCCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA
CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAA
GATTCTTTGTGCCTGCTGAAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGAT
TCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA
TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG
GGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT
CTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCCGGATAAAACAGTCATTGAATATGA
ATATGATGTCAGAACCCTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGG
AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCCG
CAAACGTTACAGTACTCATACCCCCCTCAGCTCCAAGACTTAGACCCCCCTGGCGCAGGAGCA
CACAGACTCGGAGGAGGGGCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGATCCCC
AAACTGGCAGGCTGTGTATTCCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAG
CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC
TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT
TATATGTGCAGATGGAAAACTGATGCCAACACTTCCTTTTGCCTTTGTTCCTGTGCAAC
AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTTCCAGT
TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTG
GTTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCTCTGGAGTCCAGGGGCTGGCCGGT
TGTTCTATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGG
TGGGTGT

FIGURE 62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNED
KRFFVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDKTVIEWEYDVRTTDCAGPEEQELSL
QEEVSTQGTLLESQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDGLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEW
GLYVQMEN

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
TCTGCCATGGGGCTCGGGTTGAGGGGCTGGGGACGTCCTCTGCTGACTGTGGCCACCGCCCT
GATGCTGCCCCTGAAGCCCCCGCAGGCTCCTGGGGGGCCCAGATCATCGGGGGCCACGAGG
TGACCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA
GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT
CCGCACTGGCCTGGTGGTGCTGGGCGCCACGTCTGAGTACTGCGGAGCCCACCCAGCAGG
TGTTTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGAC
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCCTGGGCCCTGCAGTGGGGCTGCTGAGGCT
GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT
TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGGCCCTGGTGTGCAGGA
ACCGGGCTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCCGAC
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTCGGCGGAGCAGTCC
CCAGCCCCGGCCCCCTGCCTGGGACCACCAGGCCCCCAGGAGAAGCCGCCTGAGCCACAACCT
TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
AAGCCTGATGTTCAAGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA
AAGGGCAGAAGCAAACCCAGTAAAATGTTAACTGACAAAAAAAAAAAAAAAAAAGAAA

FIGURE 64

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845

><subunit 1 of 1, 283 aa, 1 stop

><MW: 30350, pI: 9.66, NX(S/T): 2

MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGRF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPTQQVFGIDALTTHPDYHPMTHANDIC
LLRLNGSAVLGPAVGLLRLLPGRRARPPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLLTMLCTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA

Signal peptide:

amino acids 1-30

65/249

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA
CGCCTGTCCCCGGCCCCGGCATGAGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGCACGGTAG
CAGGCGCCGCGTGTGCTCAAGGACTATGTCACCGGTGGGGCTTGCCCCAGCAAGGCCACC
ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT
GGAAGTGGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGG
CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCCGGCACCTGGAC
TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAGATCATTGAAGAGGAGGAGCGAGT
GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCCACTGGACCACCGAGGACGGCT
TCGAGATGCAGTTTGGCGTTAACACCTGGGTCACTTTCTCTTGACAAACTTGCTGCTGGAC
AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG
GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
GCCAGAGCAAGCTCGCCATCGTCCTCTTACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT
GGTGTGACTGTCAACGCCCTGCACCCCGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG
CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA
GCCCCGAGCTGGCCGCCCAGCCCAGCACATACCTGGCCGTGGCGGAGGAAGTGGCGGATGTT
TCCGGAAAGTACTTTCGATGGACTCAAACAGAAGGCCCGCCCCCGAGGCTGAGGATGAGGA
GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCTGGTGGGCTTAGAGGCTCCCTCTGTGA
GGGAGCAGCCCCTCCCCAGATTAACCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG
ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCCTGGCACTACCTGAGCCGGGAGACCCAG
GACTGGCGGCCGCGCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGCAGTGGACTGGC
CTGCAGGTGAGCACTGCCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG
AGGGGCCATCTGATGCTTCCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC
TGTGCACTTGCAGGCCACGTCAGGAGAGCCAGCGGTGCCTGTCGGGGAGGGTTCCAAGGTGC
TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT
TGTGCATGCATGGTCCTCTCTGAGCCTTGGTTTCTTCAGCAGTGAGATGCTCAGAATAACTG
CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG
GGTGTGTTGCTGAGGGCTTCCTGTGCCAGAGCCCAGCCAGAGAGCAGGTGCAGGTGTCATCCC
GAGTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA
TTGCCTGGGACTCCCACCTTCCTATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAAC
TTGCTCATTT

66/249

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVLDILINN
AGVMRCPHWTTEDGFEMQFGVNHLLGHFLLTNLLLDKLGASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAEAEDEEVARRLW
AESARLVGLEAPSVREQPLPR

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTTCGCGAGCGCTGGCATGTGGTTCCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG
GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC
CAGCGTGGCGCGCGCCCTGGCGCCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC
GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCAT
GAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCACTTTACTCTCATCAAACGCCTGCA
GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG
GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTT
TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA
CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC
ATTCCATGGCTGGAGGAGGCTGTCACTCTCTTCCGAGGATCTTACGGAGAGTGGAAGACAGA
GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCAGGAA
ATGTTTTCTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCCAGATAATAAGAGG
ATGGCCAGGAATGTCTTGAAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGC
TGAGGCTGTCATCCAGAGGCCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC
TATGTCAGACCCTGGGTTCCCAGCCCCTCTCTACCAGATCCCTAGCCTCTACTGTTCTAT
GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTATCCACCTGGA
GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAAC
TTGCAGAACCATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG
TACCGCATCAGCAAAAGTGCCCTGGCTGAAGGACACTGTTGACCCAAAAGTGGTGAACCTCAA
CCACCGCATTGCTGCCCTCACAGGCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG
TGGTGAACCTATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCACCAAGC
AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC
GGTGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA
ATGCAGCACTGTTTTGGTGAACCTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT
GCTGGCTGTCTGTCTGGTGGGAGATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGG
ACAGGAATTCCGCAGACCCTGCAGCTCCAGCCCTGAAGACTGAACTGTTGGCAGAGAGAAGC
TGGTGGAGTCCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA
AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTGAGCTTTGTCTGTGCCTCGCAAATCAGAGGC
AAGGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA
GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGG
AGTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTTCGATCAGTGGGTC
TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG
GGGCTAGCCTGACTCCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGCAGCCCCAAG
CAGGGAGTGTCCCCCTCCCAGAAAGCATATCCCAGATGAGTGGTACATTATATAAGGATTTTT
TTTAAGTTGAAAACAACCTTTCTTTTCTTTTGTATGATGGTTTTTTTAACACAGTCATTAAAA
ATGTTTATAAATCAAAA

68/249

FIGURE 68

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERLLGLLRRYLRGEEARL
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ
VGKVAYDMGDYYHAI PWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHLQTRDITYEGLCQTLGS
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGGTTTAAAGTTCCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAG
GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAG
CGCCCAGGATGCCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTTCTGGCTGATTGGGGCCCTGGTCCT
GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCTTGAAAGTGCCTTCC
TGGCTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTCATGTTTCATGGTCTCCTTCATTGGT
GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTTCATGTACATCCTTGGGAT
CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG
ACTTCCTGAACGACAACATTTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAA
AACATCATGGACTTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
GAGCAAGAATCAGTACCACGACTGCAGTGGCCCTGGACCCCTGGCCTGTGGGGTGCCCTACA
CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAACTATCGAC
AAGGAGCGTTTTAGTGTGCAGGATGTCTACGTGCGGGGCTGCACCAACGCCGTGATCAT
CTGGTTCATGGACAACACTACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT
TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC
TCTGTCACTGATGGGCTCCTGGGGCCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG
ATGCTGCTTGTGCTACCCCAATTAGGGCCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCCCTCTGCCCACA
CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCCTGTGTGTAGGTCCCACGGCCTCTGCCTC
CCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGCTTTCCCCGAGGCAGCTCTGGAATCTGT
GCCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA
GAGCCTGAGGCTCTGCTCAGGGCCCATTTTCATCTCTGGCAGTGCCTTGGCGGTGGTATTCAA
GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCCCTCGGGGCAGGAGGGAAGG
GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTGGC
CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCCTTGAGCCTA
GTTTTTTTTTACGTGATTTTTGTAAACATTATTTTTTTGTACAGATAACAGGAGTTTCTGAC
TAATCAAAGCTGGTATTTCCCCGCATGTCTTATTCTTGCCCTTCCCCCAACCAGTTTGTAA
TCAAACAATAAAAACATGTTTTGTTTTGTTTTTAAAAA

70/249

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863

><subunit 1 of 1, 294 aa, 1 stop

><MW: 33211, pI: 5.35, NX(S/T): 3.

MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP
AIIILILLGVVMFMVSFIGVLASLRDONLYLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFL
NDNIRRGIE NYDDLD FKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPG PLACGV PYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAV IWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDG LLGPGAKPSVEAAGTGCCLCYPN

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

71/249

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA
CACCTGGGAAGATGGCCGGCCCGTGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACC
TTGATCCAAGCCACCCTCAGTCCCAGTTCATCCTCGGCCCCAAAAGTCATCAAAGA
AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC
GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA
GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
ACACGCCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATC
CGCATGGACACCAGTGCAAGTGGCCCCACCCGCCTGGTCCCTCAGTGAAGTGTGCCACCAGCCA
TGGGAGCCTGCGCATCCAAGTGTGTATAAGTCTCCTTCCTGGTGAACGCCTTAGCTAAGC
AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG
ATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTT
CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATT
AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC
TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCGTTCAGCCTCATCGTGAGTCA
GGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCCCTGTTGG
ACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG
GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT
TTTTATAGACCAAGGCCATGCCAAGGTGGCCCCAACTGATCGTGCTGGAAGTGTTCCTCCCA
GTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC
ACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
ACTCCATCCTGTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCAATTGGTG
AAGGCCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCC
AGCCTCCTTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG
GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT
CAATAAACACTTGCTGTGAAAAA

72/249

FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLLSAM
REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITQLYL
GAKLLDSQGKVTWKWFNNSAASLTMPITLDNIPFSLIVSQDVVKAABAVALSPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGLIEASSEAQFYTKGDQLILNLNLISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSQVPSLVKALGFEEAESSLTKDALVLT PASLWKPPSPVSQ

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

73/249

FIGURE 73

GAGCGAAC**ATG**GCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG
CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCCAAAGAAAGAAGGAGATGGTGTTATCTGA
AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA
AGTTCCGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
CTCCAACCTGCATAGACAGTGTGTCGTTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC
AAACTCCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTTTGGCATGGTGGATTTTG
ATGAAGGCTCTGATGTATTTTCAGATGCTAAACATGAATTCAGCTCCAACCTTTCATCAACTTT
CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTTCAGC
TGAGCAGATTGCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC
CAAATTATGCTGGTCCCCTTATGTTGGGATTGCTTTTTGGCTGTTATTGGTGGACTTGTGTAT
CTTCGAAGAAGTAATATGGAATTTCTCTTTAATAAAACTGGATGGGCTTTTGCAGCTTTGTG
TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCC
ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTA
GCTGAAACACACATTGTTCTTCTGTTAATGGTGGAGTTACCTTAGGAATGGTGCTTTTATG
TGAAGCTGCTACCTCTGACATGGATATTGGAAAGCGAAAGATAATGTGTGTGGCTGGTATTG
GACTTGTTGTATTATTCTTCAGTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC
CCATACAGCTTTCTGATGAGT**TAAAA**AGGTCCCAGAGATATATAGACACTGGAGTACTGGAA
ATTGAAAAACGAAAATCGTGTGTGTTTGAAAAGAAGAATGCAACTTGTATATTTTGTATTAC
CTCTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAAAGAAGATGTGTAGTGCCTTA
ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTT
CCCAGTGAACCTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAATTGTAAAA
CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAACTACTTTAGTTAACTTGGTCATCTGAT
TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCACATATGCC
TGTTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTGTGTGGATGTGTAT
ACTTTACGCATCTTTCCTTTTGAGTAGAGAAATTATGTGTGTCATGTGGTCTTCTGAAAATG
GAACACCATTCTTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT
GCATATTTCCCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA
TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTAACTACCTTGTATTTAGAAA
GATTTCAAGATTCATTCCATCTCCTTAGTTTTCTTTTAAGGTGACCCATCTGTGATAAAAATA
TAGCTTAGTGCTAAAATCAGTGTAACCTTATACATGGCCTAAAATGTTTCTACAAATTAGAGT
TTGTCACCTTATTCCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC
GAGGTCAGGAGTTCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATAT
AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC
GAGAATCACTTGAACTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCACTCC
AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

FIGURE 74

MAARWRFWCVSVTMVVALIVCDVPSASAQRKKEMVLSEKVSQLMEWTKRPVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFFINFPKGGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLMVLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

75/249

FIGURE 75

AAGCAACCAAAGCTGCAAGCTTTGGGAGTTGTTTCGCTGTCCCTGCCCTGCTCTGCTAGGGAGA
GAACGCCAGAGGGAGGCGGCTGGCCCGGCGGCAGGCTCTCAGAAACGCTACCGGCGGATGCTA
CTGCTGTGGGTGTGCGGTGGTTCGACGCTTGGCGCTGGCGGTACTGGCCCCGGAGCAGGGGA
GCAGAGGCGGAGAGCAGCCAAAGCGCCCAATGTGGTGCTGGTCGTGAGCGACTCCTTCGATG
GAAGGTAAACATTTTCATCCAGGAAGTCAGGTAGTGAACTTCCTTTTATCAACTTTATGAAG
ACACGTGGGACTTCCTTTCTGAATGCCTACACAACTCTCCAATTTGTTGCCCATCACGCGC
AGCAATGTGGAGTGGCCTCTTCACTCACTTAACAGAATCTTGGAATAATTTAAGGGTCTAG
ATCCAAATTATACAACATGGATGGATGTCATGGAGAGGCATGGCTACCGAACACAGAAATTT
GGGAACTGGACTATACTTCAGGACATCACTCCATTAGTAATCGTGTGGAAGCGTGGACAAG
AGATGTTGCTTTCTTACTCAGACAAGAAGGCAGGCCCATGGTTAATCTTATCCGTAACAGGA
CTAAAGTCAGAGTGATGGAAAGGGATTGGCAGAATACAGACAAAGCAGTAACTGGTTAAGA
AAGGAAGCAATTAATTACACTGAACCATTTGTTATTTACTTGGGATTAAATTTACCACACCC
TTACCCCTCACCATCTTCTGGAGAAAATTTGGATCTTCAACATTTACACATCTCTTTATT
GGCTTGAAAAGTGTCTCATGATGCCATCAAAATCCCAAAGTGGTCACCTTTGTCAGAAATG
CACCTGTAGATTATTACTCTTCTTATACAAAAAAGTGCCTGGAAGATTTACAAAAAAGA
AATTAAGAATATTAGAGCATTTTATTATGCTATGTGTGCTGAGACAGATGCCATGCTTGGTG
AAATTATTTTGGCCCTTCATCAATTAGATCTTCTTCAGAAAATATTGTCATATACTCCTCA
GACCATGGAGAGCTGGCCATGGAACATCGACAGTTTTATAAAATGAGCATGTACGAGGCTAG
TGCACATGTTCCGCTTTTGATGATGGGACCAGGAATTAAAGCCGGCCTACAAGTATCAAATG
TGGTTTCTCTTGTGGATATTTACCCTACCATGCTTGATATTGCTGGAATTCCTCTGCCTCAG
AACCTGAGTGGATACTCTTTGTTGCCGTTATCATCAGAAACATTTAAGAATGAACATAAGT
CAAAAACCTGCATCCACCCTGGATTCTGAGTGAATTCCATGGATGTAATGTGAATGCCTCCA
CCTACATGCTTCGAACTAACCCTGGAATATATAGCCTATTTCGGATGGTGCATCAATATTG
CCTCAACTCTTTGATCTTTCTCGGATCCAGATGAATTAACAAATGTTGCTGTAAATTTCC
AGAAATTACTTATTCTTTGGATCAGAAGCTTCATTCCATTATAAACTACCCTAAAGTTTCTG
CTTCTGTCCACCAGTATAATAAAGAGCAGTTTATCAAGTGGAAACAAAGTATAGGACAGAAT
TATTCAAACGTTATAGCAAATCTTAGGTGGCACCAGACTGGCAGAAGGAACCAAGGAAGTA
TGAAATGCAATTGATCAGTGGCTTAAAACCCATATGAATCCAAGAGCAGTTTGAACAAAAA
GTTTAAAAATAGTGTTCTAGAGATACATATAAATATATTACAAGATCATAATTATGTATTTT
AAATGAAACAGTTTTTAATAATTACCAAGTTTTTGGCCGGGCACAGTGGCTCACACCTGTAATC
CCAGGACTTTGGGAGGCTGAGGAAAGCAGATCACAAGGTCAAGAGATTGAGACCATCCTGGC
CAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGCGGTGGTGCACA
CCTATAGTCTCAGCTACTCAGAGGCTGAGGCAGGAGGATCGCTTGAACCCGGGAGGCAGCAG
TTGCAGTGAGCTGAGATTGCGCCACTGTACTCCAGCCTGGCAACAGAGTGAGACTGTGTGCG
AAAAAATAAAAAATAAATAAATAATTACCAATTTTTTCATTATTTTGTAAAGATGTAGTG
TATTTTAAGATAAAATGCCAATGATTATAAAATCACATATTTTCAAAAATGGTTATTATTTA
GGCCTTTGTACAATTTCTAACAATTTAGTGGAAGTATCAAAAGGATTGAAGCAAATACTGTA
ACAGTTATGTTCTTTAAATAATAGAGAATATAAAATATTGTAATAATATGTATCATAAAT
AGTTGTATGTGAGCATTTGATGGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

76/249

FIGURE 76

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSFGRLTFHGPSQVVKLPPFINF
MKTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLG LNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLS
EMHPVDYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY
SSDHGELAMEHRQFYKMSMYEASAHVPLMMGPGIKAGLQVSNVVS LVDIYPTMLDIAGIPL
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS
ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAI DQWLKTHMNPRAV

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
GCCTCTCTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT
GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAG
CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG
TGTGACATCTATAGCACCTTCTGGGCCTGCCCCGCTGACATCCAGGCTGCCCAGGCCATGAT
GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGCCATGAGATGCA
CAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC
ATCCTTGGAGGCCTCCTGGGATTCAATTCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGA
CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG
GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCCTGCTCATCC
CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC
TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT
ATGTG**TGA**AGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGACAG
CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGG
ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG
CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC
CCCTGCCCTAAGTCCCCAACCCCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG
ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTG
ACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG
GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
TCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCC
AGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

78/249

FIGURE 78

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886

><subunit 1 of 1, 230 aa, 1 stop

><MW: 24549, pI: 8.56, NX(S/T): 1

MASLGQLVGYILGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSSYSLTGYV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

79/249

FIGURE 79

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGC
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCCTGCAC
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCCCTTTGGCCTCACAAACGATTTTGTTG
TGAAGCTGAAGGTTCAAGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTTCCCTTGAGAAAGACATAGAAAGAAAATCAACTTTCACTAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

80/249

FIGURE 80

MVPRI FAPAYVSVCLLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYND AIVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTND FVVKLVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:

amino acids 1-25

FIGURE 81

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCTGCAGCACTGTT
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA
GTCTGCTTTGAGCAGTGCTGCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGA
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGCAGTGTGAGCTAATGGAACATCAGGGGAA
CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCCACTTCATT
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGAT
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCCTTCACCCT
TCTGTGAGATTTTCCATCATCTCAAGTTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTTATGTACTTTATAAATGAAAA

FIGURE 82

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

Signal peptide:

amino acids 1-24

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCGCAGCGCTCACTCGCTCGCACTCAG
TCGCGGGAGGCTTCCCCGCGCCGGCCGCGTCCCCGCCCGCTCCCCGGCACCAGAAGTTCCTCT
GCGCGTCCGACGGCGACATGGGGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA
TCCCTGCTCTTCGCTCTCTTCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTCGC
CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCAGAACGTCACCCCTCACCTGCAGGCTCT
TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
GGCGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCA
CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTG
GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCCTCGGAGCACAGGGT
CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACCTGTGTGGTGT
ACCCATCCTCCTCCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC
ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC
CTCCAACCGCCGTGCCCAGGAGCTGGTGGCGATGGACAGCAACATTCAAGGGATTGAAAACC
CCGGCTTTGAAGCCTCACCACTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG
TCCTATGTGGCCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTCGGAGCCCAGCAC
CCCCCTGTCTCCTCCAGGCCCCGGAGACGTCTTCTTCCCATCCCTGGACCCTGTCCCTGACT
CTCCAAACTTTGAGGTCATCTAGCCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG
GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTC
CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCCAGAAGCCCAGCCCTCAACCCCTC
TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCCTGTTCCAAGGATTTTGGGGTGCTGAG
ATTCTCCCCTAGAGACCTGAAATTACACAGCTACAGATGCCAAATGACTTACATCTTAAGAA
GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA
GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCCAGGCACCAGACACAGGGCACGGTG
GAGAGACTTCTCCCCCGTGGCCGCCTTGGCTCCCCCGTTTTGCCCCAGGGCTGCTCTTCTGTC
AGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCACTGGCCATCGCC
ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
CTGGGGCTTCCACTGCCTGCATTCCAGTCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC
ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG
ATGTTGCCCCACCCACTGGAGATGGTGCTGAGGGAGGTGGGTGGGGCCTTCTGGGAAGGTGA
GTGGAGAGGGGGCACCTGCCCCCGCCCTCCCCTACTCCCCTGCTCAGCGCGGGCC
ATTGCAAGGGTGCCACACAATGTCTTGTCACCCTGGGACACTTCTGAGTATGAAGCGGGAT
GCTATTAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

84/249

FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTWYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLDDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQ
DSENITAAALATGACIVGILCLPLILLLVYKQRQAASNRRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI
```

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

85/249

FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT
TTCCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCCTGCCCTCC
TTTCTGCCCACCGCTGCTTCCTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG
GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCTTTTCGTCTCCCTTCCTCCCGA
CTCCGCTCCCGGACCAGCGGCCTGACCCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCCTC
TCCTCCTTGCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCC
AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACT
TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT
TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG
CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAGTCCTGCC
AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTCC
CGCCTGCCCCAACCAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC
AACCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCCTGCCAGACTCCTGCTGCCAAGCCT
GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG
AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCAGC
CCCCACTGGCCTCAGCGCCCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG
GCAGCACAACTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG
AAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTG
CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
ACCCCTGCCGTCACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCAGAGGACAAA
GCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCCT
CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGG
CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAG
AGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA
AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCAC
GAAGGTCACTGGAACGTCTTCCTAGCCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGA
CAAAGTGACCAAGACATAACAAAGACCTTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT
ATTATATATTAATAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

86/249

FIGURE 86

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFP SRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGP GTPAPTGLSAPLSFI PRHFRPKGAGSTTVKIIVLKEKH
KKACVHG GKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHP EKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL V
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSPDPG
AEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

87/249

FIGURE 87

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGGCAACAGCTTGCGGCTGCGGGGAGCTCCC
GTGGGCGCTCCGCTGGCTGTGCAGGCGGCCATGGATTCCCTTGCGGAAAATGCTGATCTCAGT
CGCAATGCTGGGCGCAGGGGCTGGCGTGGGCTACGCGCTCCTCGTTATCGTGACCCCGGGAG
AGCGGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAGGAGCAGGGAGGAG
GCGGCCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA
CGTGGCCTGGAGGAAGAACTGGATGGTTGGCGGCGAAGGCGCGCCAGCGGGAGGTCACCGT
GAGACCGGACTTGCCTCCGTGGGCGCCGGACCTTGGCTTGGGCGCAGGAATCCGAGGCAGCC
TTTCTCCTTCGTGGGCCCAGCGGAGAGTCCGGACCGAGATACCATGCCAGGACTCTCCGGGG
TCCTGTGAGCTGCCGTGGGTGAGCACGTTTCCCCCAAACCCTGGACTGACTGCTTTAAGGT
CCGCAAGGCGGGCCAGGGCCGAGACGCGAGTCGGATGTGGTGAAGTGAAGAACCAATAAAA
TCATGTTCTCCAA
AAAAAAAAAA

88/249

FIGURE 88

MDSLIRKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA
TLQEAATTQENVAWRKNWMVGEGGASGRSP

Signal peptide:

amino acids 1-18

FIGURE 89

CAGGAGAGAAGGCACCGCCCCACCCCGCCTCCAAAGCTAACCCCTCGGGCTTGAGGGGAAGA
GGCTGACTGTACGTTTCCTTCTACTCTGGCACCCTCTCCAGGCTGCCATGGGGGCCCAGCACC
CCTCTCCTCATCTTGTTTCCTTTTGTTCATGGTCGGGACCCCTCCAAGGACAGCAGCACCACCT
TGTGGAGTACATGGAACGCCGACTAGCTGCTTTAGAGGAACGGCTGGCCCAGTGCCAGGACC
AGAGTAGTCGGCATGCTGCTGAGCTGCGGGACTTCAAGAACAAGATGCTGCCACTGCTGGAG
GTGGCAGAGAAGGAGCGGGAGGCACTCAGAACTGAGGCCGACACCATCTCCGGGAGAGTGGA
TCGTCTGGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCCAGCTCTGCCCTGTGTAGAGT
TTGATGAGAAGGTGACTGGAGGCCCTGGGACCAAAGGCAAGGGAAGAAGGAATGAGAAGTAC
GATATGGTGACAGACTGTGGCTACACAATCTCTCAAGTGAGATCAATGAAGATTCTGAAGCG
ATTTGGTGGCCCAGCTGGTCTATGGACCAAGGATCCACTGGGGCAAACAGAGAAGATCTACG
TGTTAGATGGGACACAGAATGACACAGCCTTTGTCTTCCCAAGGCTGCGTGACTTCACCCTT
GCCATGGCTGCCCGGAAAGCTTCCCGAGTCCGGGTGCCCTTCCCCTGGGTAGGCACAGGGCA
GCTGGTATATGGTGGCTTTCTTTATTTTGTCTCGGAGGCCTCCTGGAAGACCTGGTGGAGGTG
GTGAGATGGAGAACACTTTGCAGCTAATCAAATTCACCTGGCAAACCGAACAGTGGTGGAC
AGCTCAGTATTCCCAGCAGAGGGGCTGATCCCCCCTACGGCTTGACAGCAGACACCTACAT
CGACCTGGTAGCTGATGAGGAAGGTCTTTGGGCTGTCTATGCCACCCGGGAGGATGACAGGC
ACTTGTGTCTGGCCAAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGGACACACCA
TGTCCCAGAGAGAATGCTGAGGCTGCCTTTGTTCATCTGTGGGACCCTCTATGTCGTCTATAA
CACCCGTCTGCCAGTCGGGCCCCGCATCCAGTGCTCCTTTGATGCCAGCGGCACCCTGACCC
CTGAACGGGCAGCACTCCCTTATTTTCCCCGCAGATATGGTGCCCATGCCAGCCTCCGCTAT
AACCCCCGAGAACGCCAGCTCTATGCCTGGGATGATGGCTACCAGATTGTCTATAAGCTGGA
GATGAGGAAGAAAGAGGAGGAGGTTTGAGGAGCTAGCCTTGTTTTTTGCATCTTTCTCACTC
CCATACATTTATATTATATCCCCACTAAATTTCTTGTTTCCTCATTCTTCAAATGTGGGCCAG
TTGTGGCTCAAATCCTCTATATTTTGTAGCCAATGGCAATCAAATTCCTTTCAGCTCCTTTGTT
TCATACGGAACCTCCAGATCCTGAGTAATCCTTTTAGAGCCCGAAGAGTCAAACCCCTCAATG
TTCCCTCCTGCTCTCCTGCCCCATGTCAACAAATTCAGGCTAAGGATGCCCCAGACCCAGG
GCTCTAACCTTGATGCGGGCAGGCCAGGGAGCAGGCAGCAGTGTTCTTCCCCTCAGAGTG
ACTTGGGGAGGGAGAAATAGGAGGAGACGTCCAGCTCTGTCTCTCTTCCCTCACTCCTCCCT
TCAGTGTCCTGAGGAACAGGACTTTCTCCACATTGTTTTGTATTGCAACATTTTGCATTAAA
AGGAAAATCCACAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

90/249

FIGURE 90

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLILFLLSWSGPLQGQQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVRVFPFWVGTGQLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTQ
QWDTPCPRENAEAAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEEV

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

91/249

FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG
AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCAT
CCGTACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGG
CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCCTGTC
TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCCTCAGGGGCCAGTTCTCTAGCGTGG
TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG
ACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC
TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAAGGCCA
TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCCTCTCATTTCCATCACGGGATATGTT
GATAGAGACATCCAGCTACTCTGTCAGTCCTCGGGCTGGTTCCCCCGGGCCACAGCGAAGTG
GAAAGGTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG
CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGA
GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCAGTGGAATAATCCAGGCGGAACCTGGAC
TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGAC
TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACCTGTAACCCATA
GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT
TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG
GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG
ATCATGGGTACTGGGTCCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT
TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTTGACTATGAGTG
TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGT
TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCCC
ATAGTCATCTGCCCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC
AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTTCCTCCCCAGGG
GTGAAATGTAGGATGAATCACATCCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCA
GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC
ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT
AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG
TCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA
AAAAAA

FIGURE 92

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSS
VVHLYRDGKDQPFMQMPQYQGR TKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQK
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPQGQDLSTDSRTNRDMH
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRKEYVTLS
PDHGYWVLRNLNGEHL YFTLNPRFISVFPRTPTTKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSSESSQATTPFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGCGCCCGGTGGCGGTGGCGGGCGGCGGTTGCGGAGGCTTCCTTGGTGCGATTGCA
ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC
CATGAGGAGCCTGCCGAGCCTGGGCGGCCTCGCCCTGTTGTGCTGCGCCGCCGCCGCCGCCG
CCGTGCGCTCAGCCGCCTCGGCGGGGAATGTACCGGTGGCGGCGGGGCCGCGGGCAGGTG
GACGCGTCGCCGGGCCCCGGGTGCGGGGCGAGCCAGCCACCCCTTCCTAGGGCGACGGC
TCCCACGGCCAGGCCCGAGGACCGGGCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG
CGACTTCTCCAGCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCTCTTCC
ACCACCTTTCAGGCGCCGCTCGGCCCTCGCCGACCACCCCTCCGGCGGCGGAACGCACTTC
GACCACCTCTCAGGCGCCGACCAGACCCGCGCCGACCACCCCTTCGACGACCCTGGCCCGG
CGCCGACCACCCCTGTAGCGACCACCGTACCGGCGCCACGACTCCCCGGACCCCGACCCCC
GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCCCCACCCACCTGCCACCGAGGCCCCCTC
TTCGCCTCCTCCAGAGTATGTATGTAAGTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
GCAACCAGACCACAGGGGAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACC
TGCAAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTCAGCCATGTGACTGTAGTCC
ACATGGAGCTCTCAGCATACCGTGCAACAGGTAAGCAACAGAGGGTGGAAGTGAAGTTTATT
TTATTTTAGCAAGGGAAAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG
GAGGATGAGGGTCATAGATTTACAAAATATTTTATATACTTTTATTCTCTTACTTTATATGT
TATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAGCACTAG
AGTCGCCAATTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAAATTATTGAAGAAT
AAATCTGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTAGAAATGTTCTT
ATGTTTATTAATATACCATTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTCTCTCTA
ATCAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCCTAATTTA
TTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTGGAGCCAAAAG
TAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGA
ATAATGTACTGTTATCTAAGCATTTGCCTTGCTACTGCACTGAAAGTAATTATCTTTGACCT
TATGTGAGGCACTTGGCTTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAAT
AATGAAAAAATAATGACAGGTTATACTCAGTGTAACTGGGTATAACCAAGATCTGCTGC
CACTTACGAGCTGTGTTCCCTTGGGCAAGTAATTTCCCTTCACTGAGCTTGTTTCTTCTCAAG
GTTGTTGTGAAGATTAAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAA
TTCTGGTTTGTTTTAAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTTAAGA
ACTTTTAGCTCCTTGACAAAGAAGTGCTTTTACTTTAGCACTAAATATTTTAAATGCTTTA
TAAATGATATTATACTGTTATGGAATATTGTATCATATTGTAGTTTATTAAAAATGTAGAAG
AGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTTGGGAGGCCAAGGCGGGTGGAT
CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCCGTCTCTACTAAA
AATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCT
GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACT
GCACTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTTAAAAA

FIGURE 94

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLSLGLGGLALLCCAAAAAASASAAGNVTTGGGGAAGQVDASPGPGLRGEPSPHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPPLWATAGPSSTTFQAPLGPSPTTPPAAERTS
TTSQAPTRPAPTTLSTTTGPAPTTPVATTVPAPTTPRTPTPDLPSNNSSVLPTPPATEAPS
SPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

95/249

FIGURE 95

TGCGGCGCAGTGTAGACCTGGGAGG**ATG**GGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG
CCCTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGC
CTGGGCTTCCTGTACAG**TAG**CAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATT
CACAGCA

96/249

FIGURE 96

MGGLLLAAFLALVSVPRQAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
LTPENNLRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAII FTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCC
CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTT
CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCTACCCCTCGCAT
GGCTGGATTTACCCTGGCCAGTAGTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGA
CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGA
AGAAGTGATGCGGGGAGATACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG
GCACCCTGGAGTCCGGCTGCCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG
GGGACACCCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCCTGGACCCCTCCACCAC
CCGCTCCTCGGTGCTCACCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC
AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCTTAC
CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG
CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC
TCACAGCCCTCAAACCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA
ATTCACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
AGAGCAAAGCCACATCAGGAGTGA CTGAGGGGGTGGTCCGGGGAGCTGGAGCCACAGCCCTG
GTCTTCCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG
GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTCAGCCT
CTCAGGGGCCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAGCT
TCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
ACAGATGAAGAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCTCCAGGCAAGGGA
GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT
ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
CCCACTGTGCCCTCCCTTTTATTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 98

MLLLLLPLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSYPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
SIKWNKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPWACEQGTPPMISWIGTSVS
PLDPSTTRSSVLTLPQPQDHGTSLTQVTFPGASVTTNKTVHLNVSYPPQNLMTVFQGDG
TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVSLSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS
CRKKSARPAAGVGDGTGIEDANAVRGSASQGPLEPWAEDSPPDQPPASARSSVGEGELQYA
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 99

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAAGACCCTGTTTCCTG
GGTGTACAGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCCAGGA
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACT
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTTAGG
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT
GGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCT
TTTCCCCCAA

100/249

FIGURE 100

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTFLFLGVTLGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL

EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH

MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

Important features:**Signal peptide:**

amino acids 1-17

101/249

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAA
TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTTCGAG
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGG
GGCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA
TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC
ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC
AGCCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCA
GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG
AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGGCCCTCTGGTCTGTAACCACTCTCTT
CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCA
CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTTTGGTTCCTGTTCCTCTGTCTTAAT
AAGAAACCCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG
CTGTCACTTAATAATCAACCTGGGGTTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTGTGTATCCCCAGCCCCA
AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

102/249

FIGURE 102

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCGISGWGSTSSPQLRLPHTLRCANITIIEHQKCENAYPGNITDTM
VCASVQEGGKDSCQGDGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTTCCTGCTGGAGCCGATGCCAAAAACCATGCATTTCTTATTCAGATTCATTGTTT
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA
GTGAAAATAGAAGTTTTGCATCGTCCAGAAAAGTCTCTAAGACAAGCAAGAAGGGAGACCT
ACTAAATGCCCATATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
CACAAAATGAAGGCCACCCCAAATGGTTTGTCTTGGTGTGGGCAAGTCATAAAAGGCCTA
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT
TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTG
AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTAAAGA
AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT
GAACTATAGCATATTTGTATTTCTACTTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA
AAACAAAGTCACTTTTCTCCAAGTTGTATTTGCTATTTTTCCCCTATGAGAAGATATTTTGA
TCTCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTGCAAACTTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

104/249

FIGURE 104

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406

<subunit 1 of 1, 222 aa, 1 stop

<MW: 25794, pI: 6.24, NX(S/T): 1

MPKTMHFLFRFIVFFYLLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY
AEGKIIPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDHGDGDFISPKEYNVYQHDEL

Important features:**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

105/249

FIGURE 105

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT
GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTACATTCC
CCTTGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAAGTCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA
TAGTTTCTTGTTTCATTTGCGGACTGCCCTCTCAGTGTTTCCTGGGATCCCCCTCCCAATAA
AGTACTTATATTCTC

106/249

FIGURE 106

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLFTFPL
ETCNARHGGSRL

Signal peptide:

amino acids 1-18

107/249

FIGURE 107

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC
AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACCATGG
GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC
CAGCCTGCGCTGCGGGGGTGTCTTATTGACCACAGGTGGGTCCTCACAGCGGCTCACTGCA
GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA
CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC
CCCTGCCCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC
ATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT
CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG
GCGGCGTCCCGGGGAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA
GTCCTTCAAGGTCTGGTGTCTCTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAACTGAC
CTGTTTCTCCACCTCCACCCCCACCCCTTAACCTTGGGTACCCCTCTGGCCCTCAGAGCACC
AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACCTTCTTGGAACCTT
TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGCAATAGTCTGGA
ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

108/249

FIGURE 108

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSV
QPLPLPNDCATAGTECHVSGWGITNHPRNPFDPDLLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATG**TCGGGCGAGCTCAGCA
ACAGGTTCCAAGGAGGGAAGGCGTTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC
GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA
GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC
TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
AAGATGATCTCAGAGGTGACAGGAGGGGTGAGTGACACTATATCCTACCGAGACTTTGTGAA
CATGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCT**TGA**
GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT
CTTGACACACTGTGATCTCTCTCTCTCATTTGTTTGGTCATTGAGGGTTTGTGTTGTGTTT
TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTCGGGGAATCC
TGAGCCTTGGGTCCCCTCCCTCTCTTCTTCCCTCCTTCCCGCTCCCTGTGCAGAAGGGCTG
ATATCAAACCAAAAACTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
CTCACTTGGAGGAACCAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
CTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCCC
AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCCACACCTCTTCT
CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG
TACCAGAAGGAACCCTCCAGTCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG
CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTG
GGGTTTGGGGGGAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC
CAGGATGGGAGAATGAGGAGTAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
CTGAGAAATACAAGGTGCTTGTCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

110/249

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEinREFLCDQKYSDEENLPEKLTAfKEKYMefDLN
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMMLGKRSAVLKLVM
MFEGKANESSPKPVGPPPERDIASLP

FIGURE 111A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGCAGAGGCAGCCTCCTCCA
GGAGCGGGGCCCTGCACACC**ATG**GGCCCCGGGTGGGCAGGGGTGCGCGCCGCGCTGCGCGCC
CGCCTGGCGCTGGCCTTGGCGCTGGCGAGCGTCTGAGTGGGCCTCCAGCCGTCGCTGCC
CACCAAGTGCTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCCTCCGCGCGGTTT
CTCGGGGCATCCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC
ACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGATCTGGAAGACAACCAGGT
CAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA
AGAATAAGCTGCAAGTCCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA
GATTTGAGTGAAAACCAGATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATCACCGATGT
GAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC
TGCGCGATTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGTCACCAGC
TTCAACCACATGCCGAAGATCCGAACCTTGCGCCTCCACTCCAACCACCTCTACTGCGACTG
CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACACTCT
GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTG
TGCCAGCCCCCCTCGGAGCCCCCATCCTGCAATGCCAACTCCATCTCCTGCCCTTCGCC
CTGCACGTGCAGCAATAACATCGTGGACTGTGAGGAAAGGGCTTGATGGAGATTCCCTGCCA
ACTTGCCGGAGGGCATCGTCGAAATACGCCTAGAACAGAACTCCATCAAAGCCATCCCTGCA
GGAGCCTTCACCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA
TATTGCTCCAGATGCCTTCCAGGGCCTGAAATCACTCACATCGCTGGTCTGTATGGGAACA
AGATCACCGAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC
AATGCCAACAAGATCAACTGCCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTT
GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCTCTGCAGT
CCATCCAGACACTCCACTTAGCCCCAAAACCATTTGTGTGCGACTGCCACTTGAAGTGGCTG
GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCGCTGCAGCAGCCGCGCCG
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCGCTGCTCAGGCTCCGAGG
ATTACCGCAGCAGGTTTCCAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCG
TGTGAGGGCACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACCTCCC
TGAATATGTACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
TCTTCAAGAAGTTGCCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG
CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACAGCT
GGAGACCGTGCACGGGCGCGTGTTCGCTGGCCTCAGTGGCCTCAAACCTTGATGCTGAGGA
GTAACCTTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCCGTGAGACTGCTG
TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTACCACGCTTGTCTCCCT
GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA
AGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCCTAGGTGCCAGAAGCCATTTTTCTC
AAGGAGATTCCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG
TAGCTGCCAGCTGAGCCGCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGGAT
GCAGCAACAAGGGGCTCCGCGCCCTCCCCAGAGGCATGCCCAAGGATGTGACCGAGCTGTAC
CTGGAAGGAAACCACCTAACAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCT
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC
ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCGTCCACGCCTTCAAC
GGGCTGCGGTCCCTGCGAGTGCTAACCCCTCCATGGCAATGACATTTCCAGCGTTTCTGAAGG
CTCCTTCAACGACCTCACATCTCTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTG
ACTGCAGTCTTCGGTGGCTGTGCGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGGCATCGCC
CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT
CCAGTGCAAAGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAGCC
CGTGCAAGAATAACGGGACATGCACCCAGGACCCTGTGGAGCTGTACCGCTGTGCCTGCCCC

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA
GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTTCTAGCTGCTCCTGCCCTC
TGGGCTTTGAGGGGAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA
AACAATGCCACCTGCGTGGACGGGATCAACAACCTACGTGTGTATCTGTCCGCCTAACTACAC
AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCCTGAGCTGAACCTCTGTACGCATG
AGGCCAAGTGCATCCCCCTGGACAAAGGATTCTAGCTGCGAGTGTGTCCCTGGCTACAGCGGG
AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCACAAGTGCCGCCACGGGGCCAGTG
CGTGGACACAATCAATGGCTACACATGCACCTGCCCCCAGGGCTTCAGTGGACCCTTCTGTG
AACACCCCCCACCCTATGGTCTTACTGCAGACCAGCCCATGCGACCAGTACGAGTGCCAGAAC
GGGGCCAGTGCATCGTGGTGCAGCAGGAGCCCACCTGCCGCTGCCACCAGGCTTCGCCGG
CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAACCTGG
CCTCCGCCAAGGTCCGACCCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC
GGCATCCTTCTCTACAAAGGAGACAATGACCCCCTGGCACTGGAGCTGTACCAGGGCCACGT
GCGGCTGGTCTATGACAGCCTGAGTTCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGA
ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCTGAACCTAGTAGTG
GACAAAGGAACTCCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG
CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCTCTCCGCCTTGCGCCAGGGCACGG
ACCGGCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG
GACTTCAAGGCCCTCCCACCACAGTCCCTGGGGGTGTCAACAGGCTGCAAGTCTTGCACCGT
GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG
GCTGGACCGGCCCACTCTGCGACCAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC
CATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG
GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCAACATG
GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGC
GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA
GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTGCTGGGGGCT
GTGGGCCCCAGTGCTGCCAGCCCACCCGAGCAAGCGGCGGAAATACGTCTTCCAGTGCACG
GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTC
CTAAGCCCCCTGCCCGCCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC
ATGTGGGACCCCCTGGTGATTCAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA
AGAGAATATTAAGTATATTGTAAAATAAACAAAAAATAGAACTTAAAAAAAAAAAAAAAAAA
AAAAAA

FIGURE 112

MAPGWAGVGA AVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN
AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNLKNKLQVL
PELLFQSTPKLTRLDLSENQIQGIPRKA FRGITDVKNLQLDNNHISCIEDGA FRALRDLEIL
TLNNNNISRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL
RGFNVADVQKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
EIRLEQNSIKAIPAGAFTQYKKLKRIDISKNQISDIAPDAFQGLKSLSLVLYGNKITEIAK
GLFDGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQSIQTLHL
AQNPFFVCDCHLKWLDYLDQNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS
SECFMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRLNDNEVSVLEATGIFKKLPN
LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV
SNDTFAGLSSVRLLSLYDNRIITTITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKRKR
IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCSNKGLR
ALPRGMPKDVTELYLEGNHLTAVPRELSALRHLLTIDLSNNSISMLTNYTFSNMSHLSTLIL
SYNRLRCIPVHAFNGLRSLRVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHDCSLRWL
SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHR FQCKGPVDINIVAKCNACLSSPCKNNGT
CTQDPVELYRCACPYSYKGDCTVPINTCIQNPCQHGGTCHLSDSHKDGFS CSCPLGFEGQR
CEINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVP ELNLCQHEAKCIPL
DKGFSCECVPGYSGLKETDNDDCVAHKCRHGAQCVDTINGYTCTCPQGFS GPFCEHPPPMV
LLQTSPCDQYECQNGAQCI VVQQEPTCRCP PGFAGPRCEKLITVNFVGKDSYVELASAKVRP
QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS
VELVTLNQTLNLVVDKGT PKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
HGCIEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVCECRPGWTGPLC
DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKND SANACSAFKCHHGQCHISD
QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRRQKGYASCATASKVPIMECRGGCGPQCCQ
PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTCCTTCCGCA
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT
CCGGCAGGCTTTGAGGATGAAGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTCTCGAGGGCTGGCCTG
GACAATTACTGGGGCTTCAGCCTTGGAACCTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTCGCCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
GACACAAGGAATGAACCTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGA AAAAAGGCTGTGAGGTTTCCTTAAACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC
GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCACTTGTCCCGTTTCCTCCCAATA
TTCCTTCTCAAACCTGGAGAGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT
TTAAATGTC

115/249

FIGURE 114

MKAAGILTTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCHVACSALITDDLTDALICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

116/249

FIGURE 115

CAGGCCATTTGCATCCCCTGTCCTTGTGTTTCGGAGCCAGGCCACACCGTCCTCAGCAGTGT
CATGTGTTAAAAACGCCAAGCTGAATATATCATGCCCCCTATTAAACTTGTACATGGCTCCC
CATTGGTTTTTTGGAGAAAAGTTCAAGCTTTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTT
AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTCAC
CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCCAATTGACTGGATAGAGGAATACA
CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA
ACATTCAAGTCCCTGTCTCACATAGACCCTGATGTCTCTATCCATCTCTAAATGTCACCAG
CTTTGACTCAGTTGTTTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC
TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG
TTATGACGAGAGAGTCTTGGAAGATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAATCTCC
CTCCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC
TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTGTTAATTCGGGTGGACCCTTGGAGT
CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCATTCTCAGAAGCA
ATAGAAAAGTTTCATCCGTGAACCTTCCCTTAAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG
AGTGAAGGAAAAATTTTCCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAAC
TGCTGGTATTAATCAGATTGTTTTTAAGATCTCCATTAAATGTCATTTTTATGGATTGTAGACC
CAGTTTTTGAAACCAAAAAAGAAACCTAGAAATCTAATGCAGAAGAGATCTTTTAAAAAATAAA
CTTGAGTCTTGAATGTGAGCCACTTTCCTATATAACCACACCTCCCTGTCCACTTTTCAGAAA
AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG
TCATTCCATGTTTCAGCAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA
TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAGTGTGTATCATTATCAA
AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCCAGATTCAAT
CCACCGAAGTGTTCACTGTCATCTGTTAGGGAATTTTTGTTTGTCTGTCTTTGCCTGGATC
CATAGCGAGAGTGCTCTGTATTTTTTTTAAGATAATTTGTATTTTTTGCACACTGAGATATAA
TAAAAGGTGTTTATCATAAAAAAAAAAAAAAAAAAAAAA

117/249

FIGURE 116

MPLLKLVHGSPLVFGKFKLFTLVSACIPVFRRLARRRKKILFYCHFPDLLLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPDVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCATGTTGGACTTCGCGATCTT
CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC
AAGCTGCAGGAATTCCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT
GTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT
CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC
ATATCAATCCCAATAAGACATCGGACCCCTTTGAAACCATGCTGAAGTCATTATTAAGGTAT
CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAAATTGTATGAAAATGGTGT
GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCTAAAGCTTTCAGAAGAATTATTAGATA
AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTTGCT
ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCTG
CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTTCTAGATGGGTCAC
TTGATAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTTCAGTCAACATATTTTCATTGACTC
CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG
CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTTAACCACCTCTGAA
GAAGTTCAAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCCTGTACTCC
AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAAACTGTTCGAACTGCCA
AACTGACTCCAGTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATTATT
CCTAGAGAGACCCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC
ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTTCCT
CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA
GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA
AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT
ATTAAAATTTTATACATTTAAAATCATTGTAAATTGATTGAGGAAAACAACCATTTAAAAA
AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTAC
TTAA

FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLLVSLGTVDVLKQHINPNKTSDFETMLKSLLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLKLSEELLDKWLSTYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQEVIRFQKNHGTWVSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILED SMIFSLASCIITAKLCTWAICFLTTSSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVLCE TVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVL
QDPNTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

120/249

FIGURE 119

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGA
GACCGCCGCCCTTGTCCTCCGAGGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC
CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT
ACAGGCCTGCCTGCCTCTCACGTTCACCCCGAGGAGTATGACAAGCAGGACATTCAGCTGG
TGGCCGCGCTCTCTGTCACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTGTCT
TCTGCAGTGGCCTTCCAGCTGTCACTGAAATGGCTTTATTCGTCACCGTCTTTGGGCTGAAA
AAGAAACCCTTCTGATTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
CCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCCCTCGGAAACTGCTTC
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA
GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA
ATTAAAAAAAAAAAA

121/249

FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 121

TCCCGGACCCTGCCGCCCTGCCACTATGTCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCCAGCACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCCAGC
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCAGCTGGGCTAC
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTTCACGGGTGC
CCACTCAGGTCACCTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG
ATCGGGTGCCACACCCCAGGCCATCCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCT
CAGGGAGCCCTGAGGTCCAACCTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCCTTGAGGGCC
CTGCTGATCCGCACCCCATTCCTCCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA
ATAAAGATGTAGCTC

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACT
GACTCGCTGCTGCTTCGTGTTCTGCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
ATGATGGTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC
CGGGTGCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCT
CCTAGGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC
CGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC
TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCAAGGGAAGATTGTGGACCATGGCAA
TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTC
GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT
GGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT
CGGCTGGTCCAGAAGGTGTGCCCAGATTACAACTACCATAGTGATACCCCCTACTACCCATC
TGGGTGACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGC
AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTTGGGCCTCAGGCAGGGAGGGGGGTGGAG
ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGTCCCAAGTG
CTGGTCCCAACCTGAAGCTGTGGAGTGAAGTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT
CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC
TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGTT
CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTG
TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC
CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCTTGTCGTGTGCTGAGCATG
GCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC
CAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT
GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCCTCCACACTAAGGCC
ACAGCCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG
CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTCTCC
CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCGGGCCGCAGA
GCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGT
GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGGAGCAGGAAATAAAGCTT
GCCCCGGGGCA

125/249

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPY
YPSG

Important features of the protein:**Signal peptide:**

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCCA
GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG
GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT
TGGTGGAAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTGCACCTAGCCGCTAG
CATCTTCCCAGACACCGGGATCCCGGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC
GGCTGCGGCTGCCCCACACGGCTCACCATGGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG
GCCGTGCTGCTGGTCCTCACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC
CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG
GCTCCTCTTCTCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCCTTCTCG
GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT
CGATCAGATCCTGGTGAATGTGGGTAATTTTTTACATTGGAGTCTGTCTTTGTAGCACCAA
GAAAAGGAATTTACAGTTTCAGTTTTCACGTGATTAAAGTCTACCAGAGCCAACTATCCAG
GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTTGCGGGGGACAAAGATGTTAC
TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA
AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCCACGTTTTCTGGCTTTCTGGTG
TTCCCCCTATAGGATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG
AGTTATTGGAAGATCATTTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG
GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG
TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTCAATTCCTGGGATTACTGAATTAGT
TACAGATGTGGAATTTTATTTGTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
AAACTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG
TGTTAATATATTGATTATATTTGTTTTTATTCCTTTGGAATTAGTTTGTTTGGTTCTTGTA
AAAACCTGGATTTTTTTTTTTCAGTAACCTGGTATTATGTTTTCTCTTAAATAAGGTAATGAA
TGGCTTGCCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAAAA
GAATGCTTCATAGTTGTATTTTAATTGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT
TTCTAAGAAGAAGAATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG
TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCCTCCGAGGGAAATCTTATACTTTATTGC
TCAACTTTAATTAAAATGATTGATAATAACCACTTTATTAAAAACCTAAGGTTTTTTTTTTT
TCCGTAGACATGACCACTTTATTAACCTGGTGGTGGGATGCTGTGTTTCTAATTATACCTAT
TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA
TATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGCAATAT
CTTGTCTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGTCTGTTATAGAATAAAGA
TTAATATATGTTAAAAAA

127/249

FIGURE 126

MSGRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSNPATDSKGSSSSPLGI
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVFVAPRKGIYSFSF
HVIKVYQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

FIGURE 127

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC
TTTCTTCTGGTTGGTGTCTCTACTGATTCGTCCTTGTTGGTTCATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCCAGGTGAGACAGCACCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG
CCAGGCACAGTGGGCATTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGAC
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGATGGCTGTGAGAAGA
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCATGGGCAC
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
ACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGATTAACCTCAGGGAACCAGCACTTCCCAA
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTG
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

129/249

FIGURE 128

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLGPSTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKCLLCQDKN
FLLYNQRSR

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

130/249

FIGURE 129

CGGCAACCAGCCGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCCATGTTTCGCTCTGGGCTTGCCCTTCT
TGGTGCTCTTGGTGCCCTCGGTCGAGAGCCATCTGGGGGTTCTGGGGCCCAAGAACGTCCTCGCAGAAAGACGCCG
AGTTTGAGCGCACCTACGTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACCATACTGTGACCC
GCAACAGGACAGAGGGCGTGCGTGTGTCTGTGAACGTCCTGAACAAGCAGAAGGGGGCGCCGTTGCTGTTTGTGG
TCCGCCAGAAGGAGGCTGTGGTGTCTTCCAGGTGCCCTTAATCCTGCGAGGGATGTTTCAGCGCAAGTACCTCT
ACCAAAAAGTGGAAACCAACCTGTGTGAGCCCCCACCAGAATGAGTCGAGATTCAAGTTCTTCTACCTGGATG
TGTCCACCTGTCAACAGTCAACACCACATACAGCTCCGGGTGAGCCGATGGACGATTTGTGTCTCAGGACTG
GGGAGCAGTTTCAATACCAACAGCAGCAGCCCCAGTACTTCAAGTATGAGTTCCCTGAAGGCGTGGACT
CGGTAATTGTCAAGGTGACCTCCAACAAGGCTTCCCTGCTCAGTCATCTCCATTAGGATGTGCTGTGTCTG
TCTATGACCTGGACAACAACGTAGCCTTTCATCGGCATGTACCAGACGATGACCAAGAAGGCGGCCATCACCGTAC
AGCGCAAAGACTTCCCGAGCAACAGCTTTTATGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCCGGGGCT
CCCTGCCCTTCTACCCCTTCCGAGAAGATGAACCGGTGATCAAGGGCACCGCCAGAAAACCTGTGAGTGTGG
TGTCTCAAGCAGTCAGTCTGAGGCATACGTGAGTGGGATGCTCTTTGCTGGGTATATTCTCTCCTTTTACC
TGCTGACCGTCTCTGCGCTGTGGGAGAATGGAGGCAGAGAAGAAGACCTGCTGGTGGCCATTGACCGAG
CCTGCCAGAAAAGCGGTCAACCTCGAGTCTGGTGTGATTCTTTCTGGCAGTTCCCTTATGAGGGTTAGAACT
ATGGCTCCTTTGAGAATGTTTCTGGATCTACCGATGCTGGTTGACAGCGCTGGCACTGGGGACCTCTCTTACG
GTTACCAGGGCGCTCCTTTGAACCTGTAGGTACTCGGCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGATG
ACTACGACACATTGACCGACATCGATTCCGACAGAATGTCTTCGCACCAAGCAATACCTCTATGTGGCTGACC
TGGCAGCGAAGGACAAGCGTGTCTGCGGAAAAGTACCAGATCTACTTCTGGAACATTGCCACCATTTGCTGTCT
TCTATGCCCTTCTGTGGTGCAGCTGGTGATCACTACCAGACGGTGGTGAATGTACAGGGAATCAGGACATCT
GCTACTACAACCTCCTCTGCGCCCAACCACTGGGCAATCTCAGCGCCTTCAACAACATCCTCAGCAACCTGGGGT
ACATCCTGCTGGGGCTGCTTTTCTGCTCATCATCTGCAACGGGAGATCAACCACAACCGGGCCCTGCTGCGCA
ATGACCTCTGTGCCCTGGAATGTGGGATCCCCAAACACTTTGGGCTTTTCTACGCCATGGGCACAGCCCTGATGA
TGGAGGGGCTCTCAGTGCTTGTATCATGTGTGCCCCAACATATACCAATTTCCAGTTTGACACATCGTTTCTGT
ACATGATCGCCGGACTCTGCATGCTGAAGCTCTACCAGAAGCGGCACCGGACATCAACGCCAGCGCCTACAGTG
CCTACGCTGCTGCGCCATTGTCTATCTTCTCTGTGCTGGGCGTGGTCTTTGGCAAAGGGAACACGGCGTCT
GGATCGTCTTCTCCATCATTCACATCATCGCCACCTGCTCCTCAGCAGCGAGCTCTATTACATGGGCCGGTGA
AACTGGACTCGGGGATCTTCCGCCGATCCTCCACGTGCTCTACACAGACTGCATCCGGCAGTGCAGCGGGCCGC
TCTACGTGGACCGCATGCTGCTGCTGGTCACTGGGCAACGTCACTCAACTGGTGGTGGCTGCTGCTATGGGCTTATCA
TGCGCCCCAATGATTTGCTTCTTACTTGTGGCCATTGGCATCTGCAACCTGCTCCTTTACTTGCCTTCTACA
TCATCATGAAGCTCCGGAGTGGGGAGAGGATCAAGCTCATCCCTGCTCTGCATCGTTTGACCTCCGTGGTCT
GGGGCTTCCGCGCTCTTCTTCTTCCAGGGACTCAGACCTGGCAGAAAACCCCTGCAGAGTCGAGGGAGCACA
ACCGGGACTGCATCCTCCTCGACTTCTTTGACGACCACGACATCTGGCACTTCTCTCCTCCATCGCCATGTTCTG
GGTCTTCTGGTGTGCTGACACTGGATGACGACCTGGATACTGTGACGCGGGAAGATCTATGTCTTCTAGC
AGGAGCTGGGCCCTTCGCTTCACTCAAGGGGCCCTGAGCTCCTTTGTGTCTAGACCGGTCACTCTGTCTGCT
GTGGGGATGAGTCCCAGCACCGCTGCCAGCACTGGATGGCAGCAGGACAGCCAGGTCTAGCTTAGGCTTGGCCT
GGGACAGCCATGGGGTGGCATGGAACCTTGAGCTGCCCTCTGCCGAGGAGCAGGCTGCTCCCTGGAACCCCC
AGATGTTGGCCAAATGCTGCTTCTTCTCAGTGTGGGGCTTCCATGGGCCCTGCTCTTGGCTCTCCATTT
GTCCCTTTGCAAGAGGAAGGATGGAAGGGACACCTCCCCATTTCTATGCCTTGCATTTTGGCCGCTCCTCCTCCC
ACAATGCCCCAGCTGGGACCTAAGGCCTCTTTTCTCCTCCCACTCCCACTCCAGGGCCTAGTCTGGGGCTGA
ATCTCTGTCTGTATCAGGGCCCCAGTTCTCTTTGGGCTGTCCCTGGCTGCCATCACTGCCATTCCAGTCAGCC
AGGATGGATGGGGTATGAGATTTTGGGGGTTGGCCAGCTGGTGCCAGACTTTGGTGCTAAGGCCTGCAAGGGG
CCTGGGGCAGTGGCTATTCTCTTCCCTCTGACCTGTGCTCAGGGCTGGCTCTTTAGCAATGCGCTCAGCCCAATT
TGAGAACCGCCTTCTGATTCAAGAGGCTGAATCAGAGGTCACTCTTCTATCCCATCAGCTCCAGACTGATGCC
AGCACCAGGACTGGAGGGAGAAGCGCCTCACCCCTTCCCTTCTTCTTCCAGGCCCTTAGTCTTGCCAAACCCC
AGCTGGTGGCCTTTCACTGCCATTGACACTGCCAAGAATGTCCAGGGGCAAGGAGGGATGATACAGAGTTTCA
CCCGTTCTGCCCTCCACAGCTGTGGGCACCCCACTGCTACCTTAGAAAGGGGCTTCAAGGAGGATGTGCTGTTT
CCCTCTACGTGCCAGTCTTAGCCTCGCTCTAGGACCCAGGGCTGGCTTCTAAGTTTCCGTCCAGTCTTCAAGCA
AGTCTGTGTTAGTCATGCACACATACCTATGAAACCTTGAGTTTACAAAGAATTGCCCCAGCTCTGGGCAC
CCTGGCCACCTGGTCTTGGATCCCTTCTGTCACCTGGTCCACCCAGATGCTGAGGATGGGGAGCTCAGG
CGGGCCTCTGCTTGGGGATGGGAATGTGTTTTCTCCCAACTGTTTTTATAGCTCTGCTGAAGGGCTGGG
AGATGAGGTGGGTCTGGATCTTTTCTCAGAGCTCTCCATGCTATGGTTGCATTCCGTTTTCTATGAATGAATT
TGCATTCAATAAACACCAAGACTCAAAAAAAAAAAAAA

131/249

FIGURE 130

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTGEQFSFNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFFPCSVISIQDVLCPVYDLNNAVAFIGMYQTMTKKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYPFAEDEPVDQGHRQKTL SVLV SQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLLVAIDRACPESGHPRVLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLRRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVNVTGNQDICYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRALLRNDLCALECGIPKHFGLFYAMGTALM
MEGLLSACYHVCPTYTNFQFDTSEFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFSIIHIIATLLLSTQLYYMGRWKLDSGIFRRILHVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFFQGLSTWQKTPAESREHNRDCILLDDFFDDHDIWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
TCTCTTCTTGCTTGCGAGCTGGACCAAGGGAGCCAGTCTTGCGCGCTGGAGGGCCTGTCCTG
ACCATGGTGCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGC
CCAGCCTGCAGAGCTGTCTGTGGAAGTTCAGAAAACCTATGGTGGAATTTCCCTTTTATACC
TGACCAAGTTGCCGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTCAGGGGACTCA
GGCAAGGCAACTGAGGGGCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAG
GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATG
GACATGTCTTGTTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG
CCCCATTTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC
CTTCCTCTTCCTTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT
TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG
CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC
CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG
CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
GAGAATCTCAAAGTCCTATACCCGCACCACATGGCCCAGGTACACTGGAGTGGGGGTGATGT
GCACTATCACCTGGAGAGCCATCCCCGGGACCCTTTGAAGTGAATGCAGAGGGAAACCTCT
ACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
AATTCCTATGGCGAGGACTATGCGGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA
TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC
CAGGTACTGAAGTGACTAGACTGTGACAGAGGATGCAGATGCCCCGGCTCCCCCAATTCC
CACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA
GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACA
TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT
GAAGTCGAAGTCGCAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCCAGAT
TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGCCATGCTAACAGCCA
TTGATGCTGACCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACA
GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA
GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA
AGCTGGTGGGGCCAGGCCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA
GTGATGCCACCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCC
AGCCGGCTCTTTCCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCCCTCAGGTTCT
CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGGAGGTGCACACC
GCCCAGTCCCTGCAGGGCGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCAGGA
TACAGCCCTGACTCTTGCCCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCATG
GCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGGTCCCTACAGC
TTCACCCTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTC
CCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGTGAACACATAATCCCCGTGG
TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTTCAGATGATCGTGTGCTGCTGCAAC
GTGGAGGGGCAGTGCATGCGCAAGGTGGGCCGCATGAAGGGCATGCCACGAAGCTGTGGC
AGTGGGCATCCTTGTTAGGCACCTGGTAGCAATAGGAATCTTCCTCATCCTCATTTTACCC
ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCCCTGAAGGCG
ACTGTCTTGAATGGCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC
CTGGGAGAGAGCCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCTCCAT
CTGCCCTGGGGTGGAGGCACCATCACCATCACAGGCATGTCTGCAGAGCCTGGACACCAAC
TTTATGGACTGCCCATGGGAGTGCTCCAAATGTCAGGGTGTTTGCCCAATAATAAAGCCCCA
GAGAACTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 132

MVPAWLWLLCVSVPQALPKAQPAELSVPEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
KATEGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSDFQLEPRL
GALALSPKGSTSLDHALERTYQLLVQVKMDQASGHQATATVEVSIESTWVSLEPIHLAE
NLKVLYPHHMAQVHWSGGDVHYHLESHPPGPFVEVNAEGNLYVTRELDREAQAEYLLQVRAQN
SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH
VVYQLLSPEPEDGVEGRAEQVDPTSGSVTLGVLPRLRAGQNILLVLAIDLGAEGGFSSTCE
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTE
GTFGLDWEPSGHVRLRLCKNLSYEAAPSHEVVVVVQSVAKLVGPGPGPGATATVTVLVERV
MPPPKLDQESYEASVPI SAPAGSFLLTIQPSDPI SRTLRFSLVNDSEGWLCIEKFSGEVHTA
QSLQGAQPGDTYTVLVEAQDTALT LAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
TLGPNPTVQRDWRQLQTLNGSHAYLTALHWWVEPREHIIPVVVSHNAQMWQLLRVIVCRCNV
EGQCMRKVGRMKGMPTKLSAVGILVGT LVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGACATGAGGTGGATACTGTTCAATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA
GAAAAATTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCT
TCAATCGGCCTGTGGATGTCCTGGTCCCCTCTGTCACTCTGCAGGCATTTAAATCCTTCCTG
AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA
AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATACTTCAACTACGGGG
CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCTTGAC
CTGGCGAGGAGGGTGAAGATTGGACATTCGTTTGAACACGGCCGATGTATGTACTGAAGTT
CAGCACTGGGAAAGGCGTGAGGCGGCCGGCCGTTTGGCTGAATGCAGGCATCCATTCCCGAG
AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG
GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTTGCCTGTGGCCAATCC
TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC
CTGGAAGCTCCTGCATTGGTGCTGACCCAAATAGAACTGGAACGCTAGTTTTGTCAGGAAAG
GGAGCCAGCGACAACCTTGCTCCGAAGTGTACCATGGACCCACGCCAATTCGGAAGTGGA
GGTGAAATCAGTGGTAGATTTTATCCAAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC
ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCCCAGATGCC
GAGGAACTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTGCGGCACTGA
GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG
CGTATGACAACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGC
TTCCTCCTGCCAGCTAACCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC
CATCATGGAGCATGTGCGGGACAACCTCTACTAGGCGATGGCTCTGCTCTGTCTACATTTAT
TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCTACCTGTGTGAG
TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCCCTCTCCAGCCAGCTCCCTGGAGT
CGTGTGTCTTGGCGGTGTCCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTTTGGTCTG
CTGTTTTTGTATGAGCCTTTTGTCTGTTTCTCCTTCCACCCTGCTGGCTGGGCGGCTGCACTC
AGCATCACCCCTTCTGGGTGGCATGTCTCTCTCTACCTCATTTTTTAGAACCAAGAACATC
TGAGATGATTCTCTACCCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT
GTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTTTAATTTT
TCGCAGTCTTCTGGAAAAATATTTTCTTTGAGCAGCAAAATCTTGAGGGATATCAGTGAAG
GTCTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTTGGAGACAGAGTTTGTCTTGTGGC
CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTTCAAGCA
ATTCTCCTGCCTCAGCCTCTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCTGGCTA
ATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCA
ACCTCAGGTGATCTGCCCTCCTTGGCCTCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG
TGCCGGGCGCGTCCCTCCTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCCTTAC
TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTCAGTGTG
ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCCAGGAAGGCTGGGTGAA
GTGACCATCTAAATTGCAGGATGGTGAAATTATCCCCATCTGTCTAATGGGCTTACCTCCT
CTTGGCCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTACAGGTCTAAATCACTCAT
CTGGCCTGGATAATCTCACTGCCCTGGCACATTTCCCATTTGTGCTGTGGTGTATCCTGTGT
TCCTTGTCTGTTTGT
TCTGTCTATTTTGTATCCTGGACCACAAGTTCCTAAGTAGAGCAAGAATTCATCAACCAGCT
GCCTCTTGTTCATTTACCTCAGCACGTACCATCTGTCTTTTGTGTGTGTGTGTGTGTGTGT
TTGTTTTTTTGTCTTTTACCAAACATGTCTGTAAATCTTAACCTCCTGCCTAGGATTTGTACA
GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAA

135/249

FIGURE 134

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEAYVTIEDLQALLDNEDDEMQHNEGQERSSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRPAPVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDFTQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAALKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDNL

Signal peptide:

amino acids 1-16

FIGURE 135

CAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTTGTTCCTCAAATG
GCATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCCTCTGTGCTCCAATCTACTGTGTGTC
CCCGGCCAATGCCCCCAGTGCATACCCCCGCCCTTCTCCACAAAGAGCACCCCTGCCTCAC
AGGTGTATTCCTCAACACCGACTTTGCCTTCGCTTATACCGCAGGCTGGTTTTGGAGACC
CCGAGTCAGAACATCTTCTTCTCCCTGTGAGTGTCTCCACTTCCCTGGCCATGCTCTCCCT
TGGGGCCCCACTCAGTCACCAAGACCCAGATTCTCCAGGGCCTGGGCTTCAACCTCACACACA
CACCAGAGTCTGCCATCCACCAGGGCTTCCAGCACCTGGTTCACTCACTGACTGTTCCCAGC
AAAGACCTGACCTTGAAGATGGGAAGTGCCCTCTTCGTCAAGAAGGAGCTGCAGCTGCAGGC
AAATTTCTTGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGTCTTTTCTACAGATTTCTCCA
ACCCCTCCATTGCCCAGGCGAGGATCAACAGCCATGTGAAAAAGAAGACCCAAGGGAAGGTT
GTAGACATAATCCAAGGCCTTGACCTTCTGACGGCCATGGTTCTGGTGAATCACATTTTCTT
TAAAGCCAAGTGGGAGAAGCCCTTTCACCTTGAATATACAAGAAAGAACTTCCCATTCCTGG
TGGGCGAGCAGGTCACTGTGCAAGTCCCCATGATGCACCAGAAAGAGCAGTTCGCTTTTGGG
GTGGATACAGAGCTGAACTGCTTTGTGCTGCAGATGGATTACAAGGGAGATGCCGTGGCCTT
CTTTGTCTCCTTAGCAAGGGCAAGATGAGGCAACTGGAACAGGCCTTGTCAGCCAGAACAC
TGATAAAGTGGAGCCACTCACTCCAGAAAAGGTGGATAGAGGTGTTTATCCCCAGATTTTCC
ATTTCTGCCTCCTACAATCTGGAACCATCCTCCCGAAGATGGGCATCCAAAATGCCTTTGA
CAAAAATGCTGATTTTTTCTGGAATTGCAAAGAGAGACTCCCTGCAGGTTTCTAAAGCAACCC
ACAAGGCTGTGCTGGATGTCAGTGAAGAGGGCACTGAGGCCACAGCAGCTACCACCACCAAG
TTCATAGTCCGATCGAAGGATGGTCCCTCTTACTTCACTGTCTCCTTCAATAGGACCTTCCT
GATGATGATTACAAATAAAGCCACAGACGGTATTCTCTTTCTAGGGAAAGTGGAAAATCCCA
CTAAATCCTAGGTGGGAAATGGCCTGTAACTGATGGCACATTGCTAATGCACAAGAAATAA
CAAACCACATCCCTCTTTCTGTTCTGAGGGTGCATTTGACCCCAGTGGAGCTGGATTGCTG
GCAGGGATGCCACTTCCAAGGCTCAATCACCAACCATCAACAGGGACCCAGTCACAAGCC
AACACCCATTAAACCCAGTCAGTGCCCTTTTCCACAAATTCTCCAGGTAAGTAGCTTCATG
GGATGTTGCTGGGTTACCATATTTCCATTCTTGGGGCTCCCAGGAATGGAAATACGCCAAC
CCAGGTTAGGCACCTCTATTGCAGAATTACAATAACACATTCAATAAACTAAAATATGAAT
TCAAA
AAAAAA

137/249

FIGURE 136

MASYLYGVLFAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMHQKEQFAF
GVDTELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

FIGURE 137

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCACGC
CTGAGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAG
CCTTTATCTCTTCACCTTCAAGTCCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAG
TCTTGGTACATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGC
AGAAAGGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCC
AATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGC
CACCAACTCTGGGTCCAGTGTGACCTCCAGTGGGGTCCAGCACAGCCACCATCTCAGGGTCCA
GCGTGACCTCCAATGGGGTCCAGCATAGTCACCAACTCTGAGTTCCATACAACCTCCAGTGGG
ATCAGCACAGCCACCAACTCTGAGTTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAA
CTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAC
CCTCCAGTGGGGCCAGCACAGTCCACCAACTCTGGGTCCAGTGTGACCTCCAGTGGAGCCAGC
ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGA
GTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTCCA
GTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCC
ACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCCAG
CACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGAACGACCTCCAATGGGG
CTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAAC
TCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACGAC
CTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCTAGCA
CAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCACAGCCACCAACTCTGAG
TCCAGCACAGTGTCCAGTGGGATCAGCACAGTCCACCAATTCTGAGTCCAGCACACCTCCAG
TGGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAACACAGCCA
CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGC
ACAACCTCCAGTGGGGTCCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGC
TAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACT
CTGAGTCTAGCACAGTGTCCAGTGGGATCAGCACAGTCCACCAATTCTGAGTCCAGCACAACT
TCCAGTGGGGCCAACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAAC
AGCAGCTCTGACTGGAATGCACACAACTTCCCATAGTGCATCTACTGCAGTGAAGGCAA
AGCCTGGTGGGTCCCTGGTGGCGTGGGAAATCTTCCTCATCACCTGGTCTCGGTTGTGGCG
GCCGTGGGGCTCTTTGCTGGGCTCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACAC
CTTTAACACAGCTGTCTACCACCCTCATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAG
GGAATCATGGAGCCCCCACAGGCCAGGTGGAGTCCCTAACTGGTTCTGGAGGAGACCAGTA
TCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCCCTGAGCAGCCCCGGAAGCAAG
TGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCACCCAAGACCTGGTTTCCTTTTCATTTCATC
CCAGGAGACCCCTCCAGCTTTGTTTGGATCCTGAAAATCTTGAAAGAAGGTATTCTCACC
TTTCTTGCCCTTTACCAGACACTGGAAAGAGAATACTATATTGCTCATTTAGCTAAGAAATAA
ATACATCTCATCTAACACACACGACAAAGAGAAGCTGTGCTTGCCCCGGGGTGGGTATCTAG
CTCTGAGATGAACTCAGTTATAGGAGAAAACCTCCATGCTGGACTCCATCTGGCATTCAAAA
TCTCCACAGTAAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 138

MKMQKGNVLLMFGLLLHLEAATNSNETSTTSANTGSSVISSGASTATNSGSSVTSSGVSTATI
SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE
SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT
SNGAGTATNSESSTTSSGASTATNSDSSSTVSSGASTATNSESSTTSSGASTATNSESSTTSS
GASTATNSDSSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSSTTSSEAST
ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV
SEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP
GPGGNHGAPHRPRWSPNWFWRPVS SIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
CCAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
CTGTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGC
ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC
AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
GGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA
TGCCCTAAACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC
ATGACCTGGAGGGGTTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG
GGATTTGTGAATAAACTTGATACACCA

141/249

FIGURE 140

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHGTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

Important features of the protein:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

142/249

FIGURE 141

CTCCGGGTCCCCAGGGGCTGCGCCGGGCCGGCCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
CCCCGGGGGGGGCGATGACCGTGCGCTGACCCCTGACTCACTCCAGGTCCGGAGGCGGGGGCCCCGGGGCGACTCG
GGGGCGGACCGCGGGGCGGAGCTGCCGCCCGTGAGTCCGGCCGAGCCACCTGAGCCCCGAGCCGCGGGACACCGTC
GCTCCTGCTCTCCGAATGCTGCGCACCCGCGATGGGCCTGAGGAGCTGGCTCGCCGCCCATGGGGCGCGCTGCCG
CCTCGGCCACCGCTGCTGCTGCTCCTGCTGCTGCTCCTGCTGCAGCCCGCCCTCCGACCTGGGCGCTCAGC
CCCCGGATCAGCCCTGCCCTCTGGGCTCTGAAGAGCGGGCCATTCTCAGATTGGAAGCTGAACACATCTCCAATAC
ACAGCCCTTCTGCTGAGCAGGGATGGCAGGACCTGTACGTGGGTGCTCGAGAGGCCCTCTTGCACCTCAGTAGC
AACCTCAGCTTCTGCCAGGCGGGGAGTACCAGGAGCTGCTTTGGGGTGACAGCGCAGAGAAGAAACAGCAGTGC
AGCTTCAAGGGCAAGGACCCACAGCGCGACTGTCAAACACTACATCAAGATCCTCCTGCCGCTCAGCGGCAGTCAC
CTGTTCACTGTGGCACAGCAGCCTTCAGCCCCATGTGTACCTACATCAACATGGAGAACTCACCTGGCAAGG
GACGAGAAGGGGAATGTCCTCCTGGAAGATGGCAAGGGCCGTTGTCCCTTCGACCCGAATTTCAAGTCCACTGCC
CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGAATGACCCGGCCATCTCGCGGAGC
CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCCTCAGCCTAC
ATTCTGAGAGCCTGGGAGCTTGAAGGCGATGATGACAAGATCTACTTTTCTTCAGCGAGACTGGCGCAGGAA
TTTGAGTTCTTTGAGAACACCATTTGTGTCCCGCATTTGCCCGCATCTGCAAGGGCGATGAGGTGGAGGCGGTG
CTACAGCAGCGCTGGACCTCCTCCTCAAGGCCAGCTGCTGTGCTCACGGCCCGACGATGGCTTCCCTTCAAC
GTGCTGCAGGATGTCTTACGCTGAGCCCCAGCCCCAGGACTGGCGTGACACCTTTTCTATGGGGTCTTCACT
TCCAGTGGCACAGGGGAACACAGAAGGCTCTGCCGTCTGTGCTTCAATGAAGGATGTGCAGAGAGTCTTC
AGCGGCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGCCACACCCCGG
CCTGGAGCGTGATCACCAACAGTGCCCGGGAAAGGAAGATCAACTCATCCTGCAGCTCCCAGACCGCGTGCTG
AACTTCTCAAGGACCACTTCTGATGGACGGGAGGTCCGAAGCCGATGCTGCTGCTGCAGCCCCAGGCTCGC
TACCAGCGCGTGCTGTACACCGCGTCCCTGGCCTGCACCACCTACGATGTCTCTTCTGGGCACTGGTGAC
GGCCGGCTCCACAAGGCACTGAGCGTGGGCCCCGGGTGCACATCATTGAGGAGCTGCAGATCTTCTCATCGGGA
CAGCCCGTGCAGAATCTGCTCCTGGACACCCACAGGGGGCTGCTGTATGCGGCTCACACTCGGGCGTAGTCCAG
GTGCCCATGGCCAACTGCAGCCTGTACCGGAGCTGTGGGACTGCCTCCTCGCCGGGACCCCTACTGTGCTTGG
AGCGGCTCCAGCTGCAAGCAGCTCAGCCTCTACCGCCTCAGCTGGCCACCAGGCCGTGGATCCAGGACATCGAG
GGAGCCAGCGCCAAAGGACCTTTGCAGCGCGTCTTCGGTTGTGTCCCGTCTTTTGTACCAACAGGGGAGAAGCCA
TGTGAGCAAGTCCAGTTCCAGCCCAACACAGTGAACACTTTGGCCTGCCCCGCTCCTCTCCAACTGGCCGACCCGA
CTCTGGCTACGCAACGGGGCCCCCGTCAATGCCTCGGCCTCCTGCCACGTGCTACCCACTGGGACCTGTGCTG
GTGGGCACCCAAACAGCTGGGGGAGTTCCAGTGTGCTGCTACTAGAGGAGGGCTTCCAGCAGCTGGTAGCCAGCTAC
TGCCCGAGAGGTGGTGGAGGACGGGGTGGCAGACCAACAGATGAGGGTGGCAGTGTACCCGTCATTATCAGCACA
TCGCGTGTGAGTGACACAGCTGTGGCAAGGCCAGCTGGGGTGACAGACAGTCTACTGGAAGGAGTTCTTGCTG
ATGTGCAAGCTCTTTGTGCTGGCGTGCTGCTCCAGTTTTATTTCTGCTCTACCGGCACCGGAACAGCATGAAA
GTCTTCTGAAGCAGGGGGAATGTGCCAGCGTGACCCCAAGACCTGCCCTGTGGTGCTGCCCCCTGAGACCCGC
CCACTCAACGGCCTAGGGCCCCCTAGCACCCCGCTCGATCACCGAGGGTACCAGTCCCTGTGACAGACCCCCCG
GGGGCCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTTCGTGGAGGTATCCCCAGTG
TGCCCCCGGGCCCCGGGTCCGCTTGGCTCGGAGATCCGTGACTGTGGTGTGAGAGCTGACTTCCAGAGGACGC
TGCCCTGGCTTCAGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCTCCGCTGTGCTCTTCGTGGAAC
ACGACCGTGGTGCCCGGCCCTTGGGAGCCTTGGAGCCAGCTGGCCTGCTGCTCTCCAGTCAAGTAGCGAAGCTCC
TACCACCCAGACACCCAAACAGCCGTGGCCCCAGAGGTCTTGCCAAATATGGGGGCTGCCTAGGTTGGTGGA
CAGTGTCTCTTATGTAACTGAGCCCTTTGTTTAAAAAACAATTCCAATGTGAACTAGAAATGAGAGGGGAAGAG
ATAGCATGGCATGCAGCACACAGGCTGCTCCAGTTTATGGCCTCCAGGGGTGCTGGGGATGCATCCAAGTGG
TTGTCTGAGACAGAGTTGGAACCCCTACCAACTGGCCTCTTACCTTCCACATTATCCCGCTGCCACCGGCTGC
CCTGTCTCACTGCAGATTGAGACAGCTTGGGCTGCGTGCGTTCTGCCTTGCCAGTCAGCCGAGGATGTAGTTG
TTGCTGCGCTGCTCCACCACTCAGGACCAAGGGCTAGGTTGGCACTGCGGCCCTCACCAGGTCTTGGGCTC
GGACCCAACCTCTGACCTTTCCAGCCTGTATCAGGCTGTGGCCACACGAGAGGACAGCGCGAGCTCAGGAGAGA
TTTCGTGACAATGTACGCTTTCCCTCAGAATTGAGGAAGAGACTGTGCGCTGCCTTCTCCGTTGTTGCGTGA
GAACCCGTGTGCCCTTCCACCATATCCACCTCGCTCCATCTTTGAATCAAACACGAGGAACCTAAGTGCACC
CTGGTCTCTCCCACTCCCACTTCACTTCCATCCCTCACCTTCTCCACTCTAAGGATATCAACACTGCC
AGCACAGGGGCCCTGAATTTATGTGTTTTTATACATTTTTTAATAAGATGCACTTTATGTCATTTTTTAATAAA
GTCTGAAGAATTACTGTTTAAAAAATAA

FIGURE 142

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSMPCTYINMENFTLARDEKGNVLLEDGKGRCP
FDPNFKSTALVVDGELYTGTVSSFQGNDAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFFSETGQEFEEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFFPNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFKDHFLLMDGQVR
SRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLYQP
QLATRPWIQDIEGASAKDLCSASSVVSPSFVPTGEEKPCEQVQFQPNVTNLTACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDLLLVTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPVVIISTSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSM
KVFLKQGECAVHPKTCPVVLPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKR
PLSIQDSFVEVSPVCPRPVRVLGSEIRDSVV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCGGCGGCGGCGCGGCTACGAAGAGGACGGGGACAGGCGCGCTGCGAACCGA
GCCAGCCAGCCGAGGACGCGGGCAGGGCGGGACGGGAGCCCGGACTCGTCTGCCGCGCGCGTCTGCGCGCTCG
TGCCGCGCGCGCTCCCGCGCGCGAGCGGGAGGAGCGCGCCACCTCGCGCGCGAGCCGCGCTAGCGCGCGC
CGGGCATGGTCCCTCTTAAAGCGCAGGCCGCGGCGGCGGGGCGGGTGTGCGGAACAAAGCGCGCGCGGGG
CCTGCGGGCGGCTCGGGGGCGCGATGGGCGCGGCGGGGCGCGCGCGCGCTGCCGGGCGGGCGCTCG
CGGCGCTAGGGCGGGCTGGCCTCCGTGGGCGGGGCGAGCGGGCTGAGGGCGCGCGGAGCCTGCGGCGGCGGGC
GGCGCGGCGGCGCGCGCGGCGGGCGGAGCGGCGCGGGCATGCGCGCGCGCGCGCGCGCTGGCTCAGCGTGC
TGCTCGGGCTCGTCTGGGCTTCGTGCTGGCCTCGCGGCTCGTCTGCCCGGGCTTCCGAGCTGAAGCGAGCGG
GCCACGGCGCGCGCGCCAGCCCGAGGGCTGCCGCTCGGGCAGGCGGGGCTTCCAGGCGGCGGGGCGCGCG
GCGATGCGCGCGGGGCGAGCTCTGGCGCGCGCGGCTCGGACCCAGATGGCGGCGCGCGGACAGGAACCTTCTCT
TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCGCTGGCGCGCTACAGAACATGGTCCAAGACAA
TTCTTGGGAAAGTTCAGTTCTTCTCAAGTGAGGGTTCGTACACATCTGTACCAATTCAGTAGTGCCACTACGGG
GTGTGGACGACTCTACCCGCCCCAGAAGAAGTCCTTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA
AGTATGAATGGTTTATGAGAGCAGATGATGACGTATACATCAAGGAGACCGTCTGGAGAACTTCTGAGGAGTT
TGAACAGCAGCGAGCCCTCTTCTTGGGCGAGACAGGCTGGGCGACCGAAGAAATGGGAAACTTGGCCCTGG
AGCCTGGTGAGAACTTCTGCATGGGGGGCGTGGCGTGATCATGAGCCGGGAGGTGCTTCGGAGAATGGTGCCGC
ACATTGGCAAGTGTCTCCGGGAGATGTACACCACCATGAGGACGTGGAGGTGGGAAGGTGTGTCCGGAGGTTTG
CAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCAGCTTTTTTATGAGAATTACGAGCAGAACAAAAAGGGGT
ACATTAGAGATCTCCATAACAGTAAAATTCACCAAGCTATCACATTACACCCCAACAAAAACCCCTACCACT
ACAGGCTCCACAGCTACATGCTGAGCCGCAAGATATCCGAGCTCCGCCATCGCACAAATACAGCTGCACCGCGAAA
TTGTCTGATGAGCAAAATACAGCAACACAGAAATTCATAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCCTTCA
TGAGGTTTACGCCCCGCCAGCGAGAGGAGATTCTGGAATGGGAGTTTCTGACTGGAAAATACTTGTATTTCGGCAG
TTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCAGGGAAGCCTTGGACGACATTGTCTATGCAGGTCA
TGGAGATGATCAATGCCAACGCCAAGACCAGAGGGCGCATTTGACTTCAAAGAGATCCAGTACGGCTACCGCC
GGGTGAACCCCATGTATGGGGCTGAGTACATCTTGACCTGCTGCTTCTGTACAAAAAGCACAAAGGGAAGAAAA
TGACGGTCCCTGTGAGGAGGCGCGGTATTTACAGCAGACTTTAGCAAAATCCAGTTTGTGGAGCATGAGGAGC
TGGATGCACAAGAGTTGGCCAAGAGAATCAATCAGGAATCTGGATCCTTGTCTTTCTCTCAAATCCCTGAAGA
AGCTCGTCCCTTTTCAGCTCCCTGGGTCTGAAGAGTGGAGCACAAGAACCCAAAGATAAAAAGATAAACATACTGA
TTCTTTTGTCTGGGCGTTTCGACATGTTTGTGAGATTTATGGGAACTTTGAGAAGACGTGTCTTATCCCAATC
AGAAGCTCAAGCTCGTGGTCTGCTTTTCAATTCGACTCCAAACCTGACAAGGCCAAACAAGTTGAAGTATGA
GAGATTACCGCATTAAGTACCCTAAAGCCGACATGCAGATTTTGCCTGTGTCTGGAGAGTTTCAAGAGCCCTGG
CCTGGAAGTAGGATCCTCCAGTTTAACAATGAATCTTTGCTCTTCTTCTGCGACGTGCAGCTCGTGTGTTACTA
CAGAATTCCTTCAGCGATGTCGAGCAAAATACAGTTCTGGGCCAACAAATATATTTTCCAATCATCTTCAGCCAGT
ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCAGTGACAACCATTTTGCCTTTACTCAGAAAAGTGGCTTCT
GGAGAACTATGGGTTTGGCATCACGTGTATTTATAAGGGAGATCTTGTCCGAGTGGGTGGCTTGTATGTTTCCA
TCCAAGGCTGGGGCTGGAGGATGTGGACCTTTTCAACAAGGTTGTCCAGGCAGGTTTGAAGACGTTTAGGAGCC
AGGAAGTAGGAGTAGTCCACGTCCACCATCTGTCTTTGTGATCCCAATCTTGACCCCAACAGTACAAAATGT
GCTTGGGGTCCAAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA
GTTACAGTAAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCCTTAATGTCCAGCTTTGCTGGAAAAGACGTTTT
TAATTATCTAATTTATTTTCAAAAATTTTTTGTATGATCAGTTTTTGAAGTCCGTATACAAGGATATATTTTAC
AAGTGGTTTTCTTACATAGGACTCCTTTAAGATTGAGCTTTCTGAACAAGAAGGTGATCAGTGTGCTTTGAA
CACATCTTCTGCTGAACATTATGTAGCAGACCTGCTTAACTTTGACTTGAATGTACCTGATGAACAAAACCTT
TTTAAAAAATGTTTTCTTTTGAAGCCCTTTGCTCCAGTCTATGGCAGAAAACGTGAACATTCTGCAAAGTAT
TATTGTAACAAAACACTGTAACCTCTGGTAAATGTTCTGTTGTGATTGTTAACAATCCACAGATTCTACCTTTTGT
GTTTTGTTTTTTTTTTTACAATTGTTTTAAAGCCATTTTCAATGTTCCAGTTGTAAGATAAGGAAATGTGATAATA
GCTGTTTTATCATTGTCTTCAGGAGAGCTTCCAGAGTTGATCATTTCCTCTCATGGTACTCTGCTCAGCATGGC
CACGTAGGTTTTTTGTTTTGTTTTGTTTTGTTCTTTTTTGGAGCGGAGTCTCACTCTGTTACCCAGGCTGGAATG
CAGTGGCGCAATCTTGGCTCACTTTAACCTCCACTTCCCTGGTTCAAGCAATCCCCTGCCTTTGCCTCCCGAGT
AGCTGGGATTACAGGCACACACCACCGCCAGNTAGTTTTTTTTGTATTTTGTAGAGACGGGGTTTTCCCAT
GCAAGCCAGCTGGCCACGTAGGTTTTAAAGCAAGGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTCG
TGGTAGTTCATTTCGGCCTAAATAGAGCTGGCATTAAATTTCAAGAAGGATTTGGCATTCTCTCTTTCCTTACCCCT
CTCTTTAAAGGGTAAAATATTAATGTTTAGAATGACAAAGATGAATTATTACAATAAATCTGATGTACACAGACT
GAAACATACACACATACACCCTAATCAAACGTTGGGGAATAATGATTTGGTTTTGTTTCTTTCATCCTGTCTG
TGTATGTGGGTGGAGATGGTTTTTCACTCTTTCATTACTGTTTTGTTTTATCCTTTGTATCTGAAATACCTTTAA
TTTATTTAATATCTGTTGTTTCAAGACTCTGCCATTCTTGTAGTACCTGTAGTTAGTATTATTATGTGTATCGG
GAGTGTGTTTAGTCTGTTTTATTTGCAGTAAACCGATCTCCAAAGATTTCTTTTGGAAACGCTTTTCCCTCC

FIGURE 143B

TTAATTTTATATTCCTTACTGTTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTTGGG
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAATAG
CCTGATGCTCATTGGAAAAATAAACAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT
ATTCCTGTTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAACTTAAACACGAAAAAA

FIGURE 144

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836

><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAARGRRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAYRTWSKTIPGKVQFFSSEG
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRADDDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQREE
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNPMYGAEYILDLLLLYKKHKGKGMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFSLNSLKKLVFPQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT
QKTGFWRNYGFGITCIYKGDVLRVGGFDVSIQGWGLEDVDLFNKVVQAGLKTFRSQEVGVVH
VHHFVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACCGTTGCTGGGTGTCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
TTTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
ACGGACGACGCCTATGAAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG
TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA
CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAAATC
TAACTCTCCAAAACATGTTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA
CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA
ACTTTCCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC
ATTCTGGTCGATCAAACCAAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG
AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG
TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATAACAAGTCACCTGTCAC
CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT
CAGGTGAAACTGCGATAGAAAAACCCGAAGAGTTTGGAAGCAGCCAGAGAGTTGGAATAAT
GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACCTTCTTAGTGA
CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC
TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCA
GTAGGACGAACAAGTAATAAAATTGATGACATCGAACTGTTATTAACATGCTGTGTAATTC
TAGATCTAACTCTATGAATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAG
CTGCTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
AAAGTTTATTAAACAATAATATAAAATTTTAAACCTACTTGATATTCCATAACAAAGCTGA
TTTAAGCAAACCTGCATTTTTTTCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT
AAAAATATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA
ATTTTCATATGCACTAAAAACCTAATTTAAATAAAATTTTGGTTCAGGAAAAA

148/249

FIGURE 146

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLLPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSVPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTPISEETTTFTTGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAEOPYIENEEPEPEPEPAKQTEAPRMLPVVTSSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFKGHPESWNNDDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSL
YEYLDIKCVPPMREKAATVFNTLKNMCRSRRVTALLKVY
```

Signal peptide:

amino acids 1-19

FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG
ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCCACA
GGAATATCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA
GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT
CCTGCTCCCTCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGC GGTTCTTCAGGAATCAG
TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA
GTATCGAGGGAGAAGTGAAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGC
TAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAGTTCCTCAGATTAC
GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCAT
CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGC
CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCA
GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT
ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG
AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT
GCCCTGTGTGGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCA
GGCGGAAGCTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACG
CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA
ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAA
GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC
AAAATGTAGGGTGGTATGTGGGAGTGTGTGCGGATGACGTAGACAGGGGGAAGAACAATGTG
ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTTAC
ATTCAATCCCCATTTTATCAGCCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC
TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC
CTGCTGACATGTCAGTTTGAAGGCTTGTTGAGACCCTATATCCAGCATGCGATGTATGACGA
GGAAAAGGGGACTCCCATATTCATATGTCCAGTGTCTGCGGATGAGACAGAGAAGACCCTG
CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGC
CCCAGCTTCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGC
TGAGGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGAT
TGGCCTGACCCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA
CATTAGGTTTAGTTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC
CAGGCTCCTCATTGCTAGTCACGGACAGTGATTCCCTGCCTCACAGGTGAAGATTAAAGAGA
CAACGAATGTGAATCATGCTTGCAAGTTTGAGGGCACAGTGTGCTAATGATGTGTTTTTA
TATTATACATTTTCCACCATAAACTCTGTTTGCTTATTCCACATTAATTTACTTTTCTCTA
TACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAAGAG
GAGGTAGGATTTTTTCACTGATTCTATAAGCCCAGCATTACCTGATACCAAAACCAGGCAAAG
AAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCCCTCATTAAACACAGACACAAAAA
TTCTAAATAAAATTTTAAACAAATTAACATAAATAATTTAAAGATGATATATAACTACT
CAGTGTGGTTTGTCCACAAATGCAGAGTTGGTTTAAATATTTAAATATCAACCAGTGTAATT
CAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAAAAAAAAAA

150/249

FIGURE 148

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC
GVVMGMIIIVFFKSKGKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA
GGAAAAGAGTTTGTGGGAACCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTC
CTGGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAGAAGACCTACAA
TTACTATAGCACATTGTCAATTTACAACCTGACAACTATATGCTGAGTTTGGCAGAGAGGCTT
CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA
TCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG
AGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAACTGTAG
ATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA
GATCCTCACTCAGTTAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
TTGCTGCGGAACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAG
AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT
GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAA
GAACCCCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG
GTCTCCGGAGAATAATTGTCCATGAAAATACAAACACCCATCACATGACTATGATATTTCT
CTTGAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA
TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA
ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC
TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT
AGAAGGAAAAACAGATGCATGCCAGGGTGAAGTCTGGAGGACCACTGGTTAGTTCAGATGCTA
GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCAACAAG
CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAAGTGGTATCTA
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTTGGTGGTGGAGGCCATT
TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC
TGTTTGCTTGATGCATGTATTTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAACTTTATGTACATAGAGAAATAGATA
ATACAATATTACATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTGTGAGAATTTTGAC
TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC
AGCTCCTCTCATTTTCAGCAAATATCCATTTTCAAGGTGCAGAACAAGGAGTGAAAGAAAATA
TAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT
GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC
ACTTCATCATTTAGGAAGTATGGGAAGTAAAGTAAAGGAGTCCAGAAAGCAAGCAAGATATA
TCCTTATTTTTCATTTCCAAACAACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTGTG
ACCTATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATAT
TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 150

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYIYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSVPYTNVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWLIVLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCTGAAGGTTATATAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA
CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATTCCCG
CTGCATCAAGGCCTACCCACTGTCTCCATGCTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
CGTGACCTTCTTGGTTCCCAGAGCTCAGCCCTTGGCCCCCTCAAGACTTTGAAGAAGAGGAGG
CAGATGAGACTGAGACGGCGTGGCCGCCTTTGCCGGCTGTCCCCTGCGACTACGACCACTGC
CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGGCCTGCCTGTGCCC
AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCCGGTCTCCACTACTGG
CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCCGCTGAACGCTACGGTCCG
CAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTTATGTCGTTTGCGTAGTGGCCGCTA
ACGAGGCCGGGGCAAGCCGCGTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC
CCTGCCTTCGGGCCTTGACAGCCGCCTTGCGGTGCCGCCCAACCCCGCACTCTGGTCCACGC
GGCCGTGCGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
GCCTGCGCGATCGCTGGGGCTGCCCCGCCGAGCCGCCGCCGAGCCGCAGGGGCGCTCTTGA
AAGGGGCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG
GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG
GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT
GGCGCTTTGTTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCCCAATTTTTTTTAA
AGCGGCCAGATAATAAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

154/249

FIGURE 152

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874

><subunit 1 of 1, 238 aa, 1 stop

><MW: 25262, pI: 6.44, NX(S/T): 1

MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEAEDETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPGLSSPAQPPDPMPRMGEVRIAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA
AQKGPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRVFQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVAHAVGVGTALALLSCAALVWHFCLRDWRWGCPRRAAARAAGAL

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC
CTGCCCCGATGAGCCCCCGCGTGCCTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGG
CCCAGCGCCGACGATCGCTGCCGTTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGC
TTCTCCCTTACGGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCT
CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGA
TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC
ATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCCTTATCAT
TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACT
TTGGAAGTTTGCTTGTCAATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG
GAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTA
TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTTCAGAGAGAGTTTAAAGT
GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAATGACAGAGATGGACTGGCCCCCAGAT
TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGA
CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACAACCTGC
AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC
ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATGATGTC
CTTGAAGAATGACAACTCTCAGCACCTGTCACTGTCCCTCAGTAGAACTGTTGAAACCAAGCC
TGTCAAGAATCTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAG
GAGTTATAAAAGAAATGTCACAGAAGAAAACCACAACTTGTTTTATTGGACTTGTGAATT
TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACA
CCTAAGCATACTATTCTATGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTCAC
CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC
CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTT
CGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTT
CTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA
ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACCTTC
AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACCTAAAA
GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAA
TCTGTATAATTCAGTCGATTTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA
ATTTGTCCTGTATAGCATCATTATTTTTAGCCTTTCTCTGTTAATAAAGCTTTACTATTCTGT
CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAATTA
CCAGTGTGATACATAGGAATCATTATTCAGAAATGTAGTCTGGTCTTTAGGAAGTATTAATAA
GAAAATTTGCACATAACTTAGTTGATTGAGAAAGGACTTGTATGCTGTTTTTCTCCCAAATG
AAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAAGAA
GCAATAGTCTCCAAGTCAATATAAATCTACAGAAAATAGTGTTCTTTTTCTCCAGAAAAAT
GCTTGTGAGAAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTATTTCCTGATTA
ATATACTGTGGCAAATTACACAGATTATTAATTTTTTTACAAGAGTATAGTATATTTATTT
GAAATGGGAAAAGTGCATTTTACTGTATTTTGTGATTTTGTGTTTTATTCTCAGAATATGGAA
AGAAAATTAAATGTGTCAATAAATATTTTCTAGAGAGTAA

156/249

FIGURE 154

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWVTYEQELMVPVQ
WSDMVTILKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSLDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

157/249

FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC
TGCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
ACCGGGAGGATCACAGAGCCAGCATGTTACAGGATCCTGACAGTGATCAACCTCTGAACAGC
CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT
CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCTCATCAAGG
TGATTCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAG
CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
CCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
ACTCGGCCACAGGGAAGTGGTTCTCTGCCTGTTTCGACAACTTCACAGAAGCTCTCGCTGAG
ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA
TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTCT
TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTGTGGGAAGAGCCTGAAGACCCCCCGT
GTGGTGGGTGGGGAGGAGGCCCTCTGTGGATTCTTGGCCTTGGCAGGTGAGCATCCAGTACGA
CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCAGCCCCACT
GCTTCAGGAAACATAACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGC
AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCAA
AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCTCACTTTCTCAGGCACAGTCAGGC
CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA
TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA
GGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA
TGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCC
CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG
GGGCCCCGAGCACCCCAAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
TCTGGAAGGCTGAGCTGTAATGCTGCTGCCCCCTTGCAGTGCTGGGAGCCGCTTCCTTCCTG
CCCTGCCCCACCTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCC
CTCTGCCCCACAGCCTCAGCATTTCTTGGAGCAGCAAAGGGCCTCAATTCTGTAAAGAGACCC
TCGCAGCCCAGAGGCGCCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC
AGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA
GGAACCTTTCCCACTACTGAATGGAAGCAGGCTGTCTTGTAAGAGCCAGATCACTGTGGG
CTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAAGCCTA
CTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT
ACCTACTGTTGTTCATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT
CTGGCAAAAAAAAAA

FIGURE 156

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVLIKVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAETACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPCLSGSLVSL
HCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVC GGSILDPHWVLTAAHCFRKHTDV
FNWKVRAGSDKLGSFPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGCATCCCCAGGCTCCAG
AGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCC
TTTTCTCTTCCAAGTCTTCTGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCATGCCCA
GGGTGAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA
CTCTGCTCCTGAGTGGTGATGGAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGG
ATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTA
AGAAGAAGAGCAATGAGACACAGTGTTCACCTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACA
CCTGCGGCACCTTCGCCTTCAGCCCTGCTTGACCTTCATTGAACTTCAAGATTCTACCTGTTGCCCATCTCGG
AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATG
GGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGC
CTGTCTCAAGACCGACAACCTTCCTCGCTGGCTGCATCATGACGCTCCTTTGTGGCAGCCATCCCTTCGACCC
AGGTGCTCTACTTCTTCTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG
CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGC
TGCTCTGCACCCAGCGGGGCGAGCTGCCCTTCAACGTATCCGCCACGCGGTCTGCTCCCCGCCGATTCTCCCA
CAGTCCCCACATCTACGCAGTCTTCACCTCCAGTGGCAGGTTGGCGGGACCAAGGAGCTCTGCGGTTTGTGCCT
TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTA
CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCGAGTTGCTCAGTGGGCCCTCCTCTGATAAGGCCCTGACCT
TCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATA
CACGGCTTGCACTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTATGTACCTGGGAACCACCACAG
GGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAGAGATTGAGTGTCCCTGACC
CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCAGGAGGTCAGTGTGTTGTAGGCTTCTCAGGAGGTGTCTGGA
GGGTGCCCCGAGCCAACGTGAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCGGGACCCCACTGTGCCT
GGGACCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGG
GGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCGCCCGCAATCATTA
AAGAAGTCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCGACCTGTGAGCCTTGGCCTCTTATTATT
GGAGTCATGGCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGG
ATGGAGTTGGGGGTCTCTACCACTGCTGGGCAACTGAGAATGGCTTTTCATACCTGTGATCTCTACTGGGTGG
ACAGCCAGGACCAGACCTTGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGAGCATGTGAAGGTCCCGTTGA
CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCTACTGGCCCCACTTTGTCACTGTCACTGTCTCT
TTGCCTTAGTGCTTTCAGGAGCCCTCATATCCTCGTGGCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGG
TTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGG
AATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA
CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGCGGCCCAAGCACAGCCCTGACTAGGATGACAG
CAGCACAAAAGACCACCTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTG
ATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTAC
CCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCTC
CAGAAACACAGTGTTCAGAGACCCTAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAACATC
TAAACAATCATATGCTAACATGCCACTCCTGGAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCT
TCTCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCACTCGTGCACCGCTGACTCCCAGGAAGTC
TTTCTGAAGTCTGACCACCTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG
CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCTTTGT

160/249

FIGURE 158

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166

><subunit 1 of 1, 761 aa, 1 stop

><MW: 83574, pI: 6.78, NX(S/T): 4

MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQ
DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMI PWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFE
ETASEFDDFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGSLHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFAVLVSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVDADNNCLGTEVA

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAG
TGAGC**ATG**GCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCTGCTC
TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAGAG
GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA
CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACTTTAGG
TGGCAGAGGAAAATTTGAAAATTTATTAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC
ATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAACTTCGACATGGTGATA
GTTGAACTTTTGACTACTGTCTTTCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGC
CATTCTTTCCACTTCATTCCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTT
CAGTATTCCGTTCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTG
ATGTTCTTTAGTTTCTGCGAGGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA
GGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT
GGTTCATTAACCTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTAT
GTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGGAGAACTTCATTGC
CAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGA
ATCCGGAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG
AAGTGTCTAGTGTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTTGTGGA
CTGGCTTCTCAGAGTGACCTCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCG
GGCAGATAAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT
GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTAGTT
AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT
ACAAGTCCGCGGAGTGCTGCCAGTGTATCTGCGCTCCCACCCGCTCAGCCCCACACAG
CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTA
TGTCTTTTACAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGC
TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT
GGGGCCAGAAAGGTGAAGGAGACAT**TAA**GGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG
GCGATGTCACCATTTCTAGGGAGCTTCCCCTAGTTCTGGCAGCCCCATTCTCTAGTCCCTC
TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC
TAATTTTGGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT
CTTGTCTCCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG
GACCACTGACCCCTCAGATTTCCAGCCTTAAATCCACCTTCCTTCTCATGCGCCTCTCCGAA
TCACACCCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCC
TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCAATTTCTTTAGTTTCTGTTT
TGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTTCAGGGC
CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGGCCACAGTGAGCTCCT
TCTTGGCTGAGCAGGCATGGAGACTGAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACA
GCGTTATCTCTCCCAACCTCACTAA

162/249

FIGURE 160

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFLEETLGGRGKFENLLNVLEYLALQCSEFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP EIFKEMNNAFAHLPQGVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPRIQLFVTHGGQNSIMEAIQHGVPVMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFVLLGLTLGTLWLCCGKLLGMAVWWLRGARKVKET

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACACATACCATGTT
CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCTGAAGCTCT
GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCA
ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT
GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTTACGCGAGCCTAGAGAGGGC
AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGA
AGACCGGGGCACCTTGTGGGTTGCAGAGCCCTCAGCCATGTTGGGAGCCAAGCCACACTGGC
TACCAGGTCCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC
GGGTGGGCCCAGGAGGGGTGAGAGCCCGTCTGCTGGAGGGGGAGTGCCTGGTGGTCTGTGA
GCCTGGCCGAGCTGCTGCAGGGGGGCCCCGGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC
GAGTGGCATTTGCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC
ACCAGTGGGGCCATCTACTTCGACCAGGTCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC
CTCTGGCTCCTTCGTAGCCCTGTCCGGGGTGTCTACAGCTTCCGGTTCATGTGGTGAAGG
TGTACAACCGCCAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCATCTCAGCC
TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGGA
CCCTGGGGACCGAGTGTCTCTGCGCCTGCGTCGGGGGAATCTACTGGGTGGTTGGAAATACT
CAAGTTTCTCTGGCTTCCTCATCTTCCCTCTCTGAGGACCCAAGTCTTTCAAGCACAAGAAT
CCAGCCCTGACAACTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAG
ACTCCCTCTGGCTCCTATCCACCTCTTTGCATGGGACCCTGTGCCAAACACCCAAGTTTAA
GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTTCCACCCACCCACCCCAAGTTACC
CTCCAGCCACCTGCTGCATCTGTTCTGCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA
AGAAGGAAGATCTGCACTACTTTGCGGCCTCTGCTCCTCCGGTTCACCCACCCAGCTTCCT
GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCCACAGGAGCCCAG
ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATC
TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC
AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAAGGAAGGAGGGTGTATTG
TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
GGCTGTCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
GGTGAGTGTGTTTGTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
ACCATGGAAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAACTGCTCCAC
CTTTGAAGTTTGAACCTTTAGTCCCTCCACACTCTGACTGCTGCCTCCTTCTTCTCCAGCTCTC
TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTTTCTCCTGAT
CTGTGCTGTCTTATTCTCCTCCTTAGGCTTCTTACCTGGGATTCCATGATTCAATTCCTT
CAGACCCCTCTCCTGCCAGTATGCTAAACCCCTCCCTCTCTCTTTCTTATCCCGCTGTCCCAT
GGCCAGCCTGGATGAATCTATCAATAAAACAAGTAGAGAATGGTGGTCACTGAGACACTAT
AGAATTACTAAGGAGAAGATGCCTCTGGAGTTGGATCGGGTGTACAGGTACAAGTAGGTA
TGTTGCAGAGGAAAATAAATATCAAAGTGTATACTAAAATTAAAA

164/249

FIGURE 162

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEPVLLGECELVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVVKVYNRQTVQVSLMLNTWPFVISAFANDPDVTREAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL

Signal peptide:

amino acids 1-32

165/249

FIGURE 163

GCTGTTTCTCTCGCGCCACCACTGGCCGCCGGCCGCAGCTCCAGGTGTCTAGCCGCCCAGC
CTCGACGCCGTCCCGGGACCCCTGTGCTCTGCGCGAAGCCCTGGCCCCGGGGGCCGGGGCAT
GGGCCAGGGGCGCGGGGTGAAGCGGCTTCCCGCGGGGCCGTGACTGGGCGGGCTTCAGCC**AT**
GAAGACCCTCATAGCCGCCTACTCCGGGGTCTGCGCGGCGAGCGTCAGGCCGAGGCTGACC
GGAGCCAGCGCTCTCACGGAGGACCTGCGCTGTGCGCGAGGGGTCTGGGAGATGGGGCACT
GGATCCAGCATCCTCTCCGCCCTCCAGGACCTCTTCTCTGTACCTGGCTCAATAGGTCCAA
GGTGGAAAAGCAGCTACAGGTCATCTCAGTGCTCCAGTGGGTCTGTCCTTCTTGTACTGG
GAGTGGCCTGCAGTGCCATCCTCATGTACATATTCTGCACTGATTGCTGGCTCATCGCTGTG
CTCTACTTCACTTGGCTGGTGTGTTGACTGGAACACACCCAAGAAAGGTGGCAGGAGGTCACA
GTGGGTCCGAAACTGGGCTGTGTGGCGCTACTTTCGAGACTACTTTCCCATCCAGCTGGTGA
AGACACACAACCTGCTGACCACCAGGAATAATCTTTGGATACCACCCCCATGGTATCATG
GGCCTGGGTGCCTTCTGCAACTTCAGCACAGAGGCCACAGAAGTGAGCAAGAAGTTCCCAGG
CATACGGCCTTACCTGGCTACACTGGCAGGCAACTTCCGAATGCCTGTGTTGAGGGAGTACC
TGATGTCTGGAGGTATCTGCCCTGTGAGCCGGGACACCATAGACTATTTGCTTTCAAAGAAT
GGGAGTGGCAATGCTATCATCATCGTGGTGGGGGTGCGGCTGAGTCTCTGAGCTCCATGCC
TGGCAAGAATGCAGTCACCCTGCGGAACCGCAAGGGCTTTGTGAAACTGGCCCTGCGTCATG
GAGCTGACCTGGTTCCCATCTACTCCTTTGGAGAGAATGAAGTGTACAAGCAGGTGATCTTC
GAGGAGGGCTCCTGGGGCCGATGGGTCCAGAAGAAGTTCCAGAAATACATTGGTTTCGCCCC
ATGCATCTTCCATGGTCGAGGCCTCTTCTCCTCCGACACCTGGGGGCTGGTGCCCTACTCCA
AGCCCATCACCCTGTTGTGGGAGAGCCCATCACCATCCCCAAGCTGGAGCACCCAACCCAG
CAAGACATCGACCTGTACCACACCATGTACATGGAGGCCCTGGTGAAGCTCTTCGACAAGCA
CAAGACCAAGTTCGGCCTCCCGGAGACTGAGGTCTGGAGGTGAAC**TGAG**CCAGCCTTCGGG
GCCAATTCCCTGGAGGAACCAAGCTGCAAATCACTTTTTTGTCTGTAAATTTGGAAGTGTCA
TGGGTGTCTGTGGGTTATTTAAAAGAAATTATAACAATTTTGCTAAACCAAAAAAAAAAAAA
AAA
AAAAAAAAAAAAAAAAAAAAA

166/249

FIGURE 164

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIADVLYFTWLVFDWNTPKKGGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEESWGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTKFGLPETEVLEVN

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-
245, 318-323, 378-383

167/249

FIGURE 165

GGGCGGCGGGATGGGGGCGGGGCGGGCGGGCGCCGCACTCGCTGAGGCCCCGACGCAGGGCCGGGCGGGCCCA
GGGCCGAGGAGCGCGGGCGCCAGAGCGGGGCGGGAGGCGACGCCGGGGACGCCCGCGGACGAGCAGGTGGCG
GCGGCTGCAGGCTTGTCCAGCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCCTTGGA
CGGCTGTCTCAGCGAGGGGCGGTGCACCCGCTCCTGAGCAGCGCCATGGGCTGCTGGCCTTCCTGAAGACCCA
GTTCTGTCTGCACCTGCTGGTTCGGCTTTGTCTTCGTGGTGAGTGGTCTGGTCACTCAACTTCGTCCAGCTGTGCAC
GCTGGCGCTCTGGCCGCTCAGCAAGCAGCTCTACCGCCGCTCAACTGCCGCTCGCCTACTCACTCTGGAGCCA
ACTGGTCATGCTGCTGGAGTGGTGGTCTGCACGGAGTGTACACTGTTACGGACCAGGCCACGGTAGAGCGCTT
TGGAAGGAGCAGCAGTCATCATCCTCAACCACAACCTCGAGATCGACTTCCTCTGTGGGTGGACCATGTGTGA
GCGCTTCGGAGTGTGGGAGCTCCAAGTCTCTCGTAAGAAGGAGCTGCTCTACGTGCCCCCTCATCGGCTGGAC
GTGGTACTTTCTGGAGATTGTGTCTGCAAGCGGAAGTGGGAGGAGACCGGGACACCGTGGTCAAGGGCTGAG
GCGCTGTGGACTACCCGAGTACATGTGGTTTCTCCTGTACTGCGAGGGGACGCGCTTCACGGAGACCAAGCA
CCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGCTTCCTGTCTCAAGTACCACCTGCTGCCGCGGACCAAGGG
CTTCACCACCGCAGTCAAGTGCCCTCCGGGGGACAGTCGCAGCTGTCTATGATGTAACCCCTGAACCTCAGAGGAAA
CAAGAACCCGTCCCTGCTGGGGATCCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTGAGGAGATTTCCTCT
GGAAGACATCCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACCAGGAGAAGGACGCGCTCCA
GGAGATATATAATCAGAAGGGCATGTTCCAGGGGAGCAGTTTAAAGCTGCCCGGAGGCGGTGGACCTCCTGAA
CTTCCTGTCTGGGCCACCATTCCTGTCTCCCTCTTCAGTTTGTCTTGGGCGTCTTTGCCAGCGGATCACC
TCTCCTGATCCTGACTTTCTTGGGGTTTGTGGGAGCAGCTTCCTTTGGAGTTCGCAGACTGATAGGAGAATCGCT
TGAACCTGGGAGGTGGAGATTGCAGTGAAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT
CAGTCTCAAAAAAAAAAAAAAAAAACAAAAAACCCAGAAATTCTGGAGTTGAACCTGTGTAGTTACTGACATGAAAA
ATTCAGTAGAGGCTGAACAGCAGATTTGAGCAGGCAGAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT
TTTCAGGCTAATGAAAAAGAATGAAGGAAAATTAACAGCCTCAGAGACCCATGGTGCACCGTCACACAAATCAA
CATATGCATGATGAGAGTCCCAGAAGGAGAGGAGAGAAAGGTCAGAAAGAATGGCCACAAGCTGATGAAAAACA
GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTTCAT
AATCAAAGTGTCAAATGACAAAGAATCTTGAAAGCAGCAAGAGATGAGCAACTTATCTTGTCAAAGGATCTTTG
ATCAGATTAACAGCTCATTTCTCCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA
AACCTTCAACTGTAATTATTGGACTTTTGTAGTCTTAGATGGTCTGACCTCTTTGTCTTCAGGGACAGTTTTTCA
ATTTAATCCCTAATAACAATTAGTCAAGCTTCCTTGACCTGTAGGAAGGCTGTCTTTAGGCCGGGCACAGTGGC
TTACACCTGTAATCCAGCACTTTGGGAGGCCAGACGGGTGGATCATTTGGGGTCAGGCTGATCTCAAACCTCCT
GAGTTCAGGTGATCTGCCCCCTCAGCCTCCCAAAGTGTGTGATTGCAGGCGTGAGCCACTGCGCCTGGCCGGA
ATTTCTTTTTAAGGCTGAATGATGGGGGCCAGGCACGATGGCTCACGCCTGTGATCCCAAGTAGCTTGATTGTA
AACATGCACCACCATGCCTGGCTAATTTTTGTATTTTTAGTAGAGACGTGTAGCCAGGCTGGTCTCGATCTCCT
GACCTCAAGTGACCACCTGCCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCCTGGCCTTGA
GCATCTTGTGATGTGCTTATTGGCCATTTGTATATCTTCTATCTTCTTTGGGAAATGTCTGTTCAAGTCTTTG
CCTTTTTAAATTTTTATTATTTATTTATTTATTTTGTAGACAGGGTCTTGTCTGTTGCCAGGCTGGAGTA
CAGTGGCACAGTCTTGGCTCACTGCAGCCTCGACCTCCTGGGCTGCAGTGATCCTCCACCTCAGCCTCCCTTGT
AGCTGTATTTTTTTGTATTTTGTATTTTGTAGCTGTAGTTTTTGTATTTTTTGTGGAGACAGCATTTACCATGA
TGCCAGGCTGGTCTTGAACCTCTGAGCTCAAGTGATCTGCCTGCTTCAGCCTCCCAAAGTGTGGGATTACAGA
CATGAGCCACTGCACCTGGCAAACTCCCAAATTAACACACACACAAAAAACCACTGATTCAAAAATGGGCA
GAGGGGCCGGGTGTGGCCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTTGGGCATGAGAAGTCGAGGCTG
CAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCTGTCTC

FIGURE 166

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVG FVFVVSGLVIN FVQLCTLALWPVSKQLYRRLNCR LAYSLWSQLV
MLLEWWSCTECTLFTDQATVEREFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGVGAASFGVRRLLIGESLEPGRWRLQ

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTTATTTTAAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCA
GCCAGCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT
GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCG
GCTTACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG
GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAAATTCCTGGGATCTGCCTATACCTTCTT
TTCTCTAACCTGGCATAACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAA
AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCTGCCCCCTGGCCAGCTTCATTGT
ACATGTGGTGTCTCTTGTCTGTTCCCTGTAATGTGGTATGCCATGGGGTCTTTGCACAAGCCT
TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTC
ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
CTTGTTTAATGCTCTCATAAGACCACTTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA
TCTTTATGTGCGTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCCAGCTCTGAGC
TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT
CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA
GATGGTGTAGGGCCCAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA
TGCAGGTCTTGATTAGTAGGCCCAGGTTGGGCATCTCTAACAACTCCCACGTGATGCTGA
TGCTGGTCTATGAATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC
TCACACCTATGATCCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
TCAAGACTAGCCTGGCCAACATGGTGGAAACCCATCTGTACTAAAAATACACAAATTAGCTG
GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG
AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC
AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

170/249

FIGURE 168

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234

><subunit 1 of 1, 143 aa, 1 stop

><MW: 15624, pI: 9.58, NX(S/T): 0

MHHSLQCPGAATRHIHLCVCF SFALALGHFLLISLVGKGLSLSCGVGGRQAGLRLIRPWVRR
EGKINFYTN GDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL

Important features of the protein:**Signal peptide:**

amino acids 1-28

FIGURE 169

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAAGCCAC
AGGAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTAC
ATTAAAATCTGTTTTTTGTTCTCTTGTAAC TAGCCTTTACCTTCCTAACACAGAGGATCTGT
CACTGTGGCTCTGGCCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC
ACCGTCCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGA
GCTGCGGCTTTC AAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTT
CATAGGCGATGGCTCCCAGTGGCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG
CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCCGCCAT
CTAACCTTTTCATGTCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG
AAGCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT
TATGTGACAGGACTTGCATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA
GGGAAGGAACTTGTGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTATCACAAAGGC
ATCGAGTCTCCTGCATTCACTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT
CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTG
AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG
CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCTCCTTCCCTC
TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG
GCTCAGTGTTGGCCCAGGAGGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG
AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT
CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT
TCAAATGATCTCCAAGGGCCCTTATACCCCAGGAGACTTTGATTTGAATTTGAAACCCCAA
TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG
CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTG
GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT
GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
AAAAATAAAAAAAGAATTATGGTTATTTGTAA

172/249

FIGURE 170

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277

><subunit 1 of 1, 109 aa, 1 stop

><MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA

SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:

amino acids 1-15

FIGURE 171

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
CCGCCGCCTCCTGCCCCGCGCCATGACCCAGCCGGTGCCCCGGCTCTCCGTGCCCCGCCGCGCT
GGCCCTGGGCTCAGCCGCACTGGGCGCCGCCTTCGCCACTGGCCTCTTCTGGGGAGGCGGT
GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCCTGTGG
CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC
CCTGGAGCAGCCGCAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC
TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC
CTGGCCCTGGCCCTGGCGCTGCCCCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA
GCCCCCGAGCTGGGACGGCCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAGATCGACCTCC
GGCTGAAGCCCGCCTTGGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC
GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA
GCTGCTGCGACCCGGAGGCATCCTCGCCGTCTCAGAGTCTGTGGCGCGGGAAGGTGCTGC
AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG
GACGTCAGGGTCTACATCAGCCTCCTGCCCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT
CTAGGGCTGGCCCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCCAGGAATTGAC
CCTGAGTTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAAA

174/249

FIGURE 172

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQVPVRLSVPAALALGSAALGAFAFATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSRS
MREHPALRSLRLLTLEQPQGDSMMTCEQAQLLANLARLIQAKKALDLGTFTGYALALALAL
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDRLKPALETIDELLAAGEAGTFDVAVVDA
DKENCSAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVVRVYIS
LLPLGDGLTLAFKI

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

175/249

FIGURE 173

CCGCCGCCGAGCCGCTACCGCCGCTGCAGCCGCTTTCCGCCGCCCTGGGCCTCTCGCCGTCA
GC**ATG**CCACACGCCTTCAAGCCCCGGGACTTGGTGTTCGCTAAGATGAAGGGCTACCCCTCAC
TGGCCTGCCAGGATCGACGACATCGCGGATGGCGCCGTGAAGCCCCACCCAACAAGTACCC
CATCTTTTTCTTTGGCACACACGAAACAGCCTTCCTGGGACCCAAGGACCTGTTCCCTTACG
ACAAATGTAAAGACAAGTACGGGAAGCCCAACAAGAGGAAAGGCTTCAATGAAGGGCTGTGG
GAGATCCAGAACAACCCCCACGCCAGCTACAGCGCCCTCCGCCAGTGAGCTCCTCCGACAG
CGAGGCCCCCGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGGACGATGAGGACCGGG
GGGTCTATGGCCGTACAGCGGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA
GACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCCTGCGCTAAAGATGTC
GGTCTCGAAACGAGCCCCGAAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG
AAGAGGAGAAGCTCGGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACCAGGACTTCACACCT
GAGAAGAAAGCAGCGGTCCGGGCGCCACGGAGGGGGCCCTCTGGGGGGACGGAAAAAAAGAA
GGCGCCGTGAGCCTCCGACTCCGACTCCAAGGCCGATTCCGACGGGGCCAAGCCTGAGCCGG
TGGCCATGGCGCGGTCCGGCTCCTCCTCCTCCTTCTCCTCCTCCTCCGACTCCGATGTG
TCTGTGAAGAAGCCTCCGAGGGGAGGAAGCCAGCGGAGAAGCCTCTCCCGAAGCCGCGAGG
GCGGAAACCGAAGCCTGAACGGCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGACGAGG
TGGACCGCATCAGTGAGTGGAAGCGGCGGGACGAGGCGCGGAGGCGCGAGCTGGAGGCCCGG
CGGCGGCGAGAGCAGGAGGAGGAGCTGCGGCGCCTGCGGGAGCAGGAGAAGGAGGAGAAGGA
GCGGAGGCGCGAGCGGGCCGACCGCGGGGAGGCTGAGCGGGGACGCGGCGGCAGCAGCGGGG
ACGAGCTCAGGGAGGACGATGAGCCCGTCAAGAAGCGGGGACGCAAGGGCCGGGGCCGGGT
CCCCCGTCTCTCTGACTCCGAGCCCGAGGCCGAGCTGGAGAGAGAGGCCAAGAAATCAGC
GAAGAAGCCGAGTCTCTAAGCACAGAGCCCGCCAGGAAACCTGGCCAGAAGGAGAAGAGAG
TGCGGCCCCGAGGAGAAGCAACAAGCCAAGCCCGTGAAGGTGGAGCGGACCCGGAAGCGGTCC
GAGGGCTTCTCGATGGACAGGAAGGTAGAGAAGAAGAAAGAGCCCTCCGTGGAGGAGAAGCT
GCAGAAGCTGCACAGTGAGATCAAGTTTGCCCTAAAGGTGACAGCCCCGACGTGAAGAGGT
GCCTGAATGCCCTAGAGGAGCTGGGAACCTGACAGGTGACCTCTCAGATCCTCCAGAAGAAC
ACAGACGTGGTGGCCACCTTGAAGAAGATTGCGCGTTACAAAGCGAACAAGGACGTAATGGA
GAAGGCAGCAGAAGTCTATACCCGGCTCAAGTCGCGGGTCTCGGCCCAAAGATCGAGGCGG
TGCAGAAAGTGAACAAGGCTGGGATGGAGAAGGAGAAGGCCGAGGAGAAGCTGGCCGGGGAG
GAGCTGGCCGGGGAGGAGGCCCCCAGGAGAAGGCGGAGGACAAGCCCAGCACCGATCTCTC
AGCCCCAGTGAATGGCGAGGCCACATCACAGAAGGGGGAGAGCGCAGAGGACAAGGAGCACG
AGGAGGGTCTGGGACTCGGAGGAGGGGCCAAGGTGTGGCTCCTCTGAAGACCTGCACGACAGC
GTACGGGAGGGTCCCCGACCTGGACAGGCCTGGGAGCGACCGGCAGGAGCGCGAGAGGGCACG
GGGGGACTCGGAGGCCCTGGACGAGGAGAGCT**TAG**CGCGGGCAGCCAGGCCAGCCCCCGC
CCGAGCTCAGGCTGCCCCCTCTCCTTCCCCGGCTCGCAGGAGAGCAGAGCAGAGAAGTGTGGG
GAACGCTGTGCTGTTTGTATTTGTTCCCTTGGGTTTTTTTTCTGCCTAATTTCTGTGATT
TCCAACCAACATGAAATGACTATAAACGGTTTTTTAATGA

176/249

FIGURE 174

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61, NX(S/T): 0

MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD
KCKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDEDRG
VMAVTAVTATAASDRMESDSDSKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE
EENSESSSESEKTSQDFTPEKKA AVRAPRRGRLGGRKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSSSDSDSVKPPRRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGAEERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEAREAKKSAKKPQSSSTEPARKPGQKEKRV
RPEEKQQAQPVKVERTKRSEGFMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDS PDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEEKLAGEELAGEEAPQEKAEADKPSTDLSAPVNGEATSQKGESAEDKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLD RPGSDRQERERARGDSEALDEES

Signal peptide:

amino acids 1-13

SUBSTITUTE SHEET (RULE 26)

178/249

FIGURE 176

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

><subunit 1 of 1, 777 aa, 1 stop

><MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNI PRLKLT YKDLLLSNSCIPFL
GSSEGLDFQTLLLDEERGRLLLGA KDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFT RSLGPTHDHXYIRTDISEHYWLN GAKFIGTFF
IPDTYNPDDDKIYFFFRESSQEGSTSDKTILSRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVG VFTTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGP TFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVV SISKEKWNMEEVVLEE
LQIFKHSSIIILN MELSLKQQQLYIGSRDGLVQLSLHRC DTYGKACADCC LARDPYCAWDGNA
CSRYAPT SKRRARRQDVKYGDPITQCWDIEDSISHETADEKVI FGIEFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMY YCKAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKKRNRRHHRDLDELPRAVAT

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGCAGAGGTATCCTGGAGCATGCCACCGGGGAGCAGA
CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGTATTTTCCCCACCCAC
CTCAGCAGTTTCAGCCAGCAGGGACTGATCAGGTGTGTCTCTGGAGTGGGGAGCAGAAGGCGTGGCTGGCAAGA
GTGGCCTGGAGAAAGAGGTTGAGCGCTTGACCAGCCGAGCTGCCCGTACTACAAGATCCAGAACCATGGGCATC
GGGTGAGGTGGGGGGGCACAGGTGTCTGTGCACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG
AGCCATTGAGGGTGTCTGAGCTACAGAGGGGAGGAAAGGTATTTTAAGGTAACAGTGTGGCACAATAGTTAA
GAGCACAGTTTTTTGGAGCTAGACCGACATAGGTTCAAATTTCTTCTGTGCTTCTAGTTCTGTAGCCCCAGGT
AAGGGAGTGACTTAACCTCTCTGGACTTCAATTTCTCTCATCTAAAGTAGGGCCAATAATAGACCCACCTCAT
AGGGAAGATTAAATGACATAATGTATGTATGATGCACTAGCAAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG
TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGGCGGCAGAGGCTT
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGCATCCGCCGGGCACAGGTGAGCC
AGGTGAAGGGGGCTGCCGGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGGGCGCTCAGTGAGGCTCGGCTGTCCAGAGGGACCTCTCTC
CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCC
CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGGTATTTTCGCTATCAGGCAGGGCGTGAGGATG
AGCTGACAATCACGGAGGTGAGTGGCTGAGGTCATAGAGGAGGAGATGCTGACGAATGGGTCAAGGCTCGGA
ACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCAGAGAGCAGCC
AAGACAGTGACAATCCCTGCGGGGCAGAGCCACAGCATTCCTGGCACAGGCCCTGTACAGCTACACCGGACAGA
GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGTCTGCTGCCCGGGCCCAAGATGGAGTAGATGACG
GCTTCTGGAGGGGAGAATTTGGGGGCCGTGTGGGGTCTTCCCTCCCTGCTGGTGGAAAGAGCTGCTTGGCCCC
CAGGGCCACCTGAACTCTCTGACCCTGAACAGATGCTGCCGTCCCTTCTCTCTCCAGCTTCTCCCCACCTGCAC
CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCCCTGGACTTCCCTGGGTTCTCTGG
ACATGATGGCACCTCGACTCAGGCCGATGCTCCACCACCTCCCCCGCGGCTAAAGCCCCGGATCCTGGCCACC
CAGATCCCTCACCCTGAAGGCCAGGGAAGCCTTGACCCCAAGTGATGCTGCTGTCCCTATCTTCAAGCTGTCAGA
CCACACCATCAATGATCCAGAGCAACACAGCCAAAGCTGGAATCGCCCTTATTTCCACCCTCACCTCCAAGGGT
GGAACTTGCCCCCTTCCCATTTCTAGAGCTGGAACCCACTCCTTTTTTTCCATTGTTCTATCATCTCTAGGACC
GGAATACTACCTTCTCTTCTGTCTATGACCTATCTAGGTTGGTGAAATGCCTGAAATCTCTGGGGCTGGAAACC
ATCCATCAAGGTCTCTAGTAGTTCTGGCCACCTCTTCCCCACCTGGCTCCATGACCCACCCCACTCTGGATG
CCAGGGTCACTGGGGTTGGGCTGGGGAGAGGAACAGGCCCTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG
CTGTAATGCTCTGAGCGGATTTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCCTGGGCTCTTGTG
CTAAGAGGGCAGGGGGCTACGGTGCTATTGCTTTAGGGGGCCACCACGGGCAGGGGCTGCTCCAGCTGCCAC
GCTCTATCATATGGAGCGAGTGTTGGGGAGGGCGGGGCAGGCAGCCTGTTGCAGGCAGGGGAAGGAGAAGAGAC
TGAGGGGCTGTGACCTCTCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC
AGCTGGGGGCGAGTGCTGTCCAGTGGAGGGGAGGGCTTTTACGCCACCCACCCCTGGCCCTGCCAGCTGGTAG
TCCATCAGCACAAATGAAGGAGACTTGGAGAAGAGGAAGAATAACACTGTTGCTTCTGTTCAAGCTGTGTCCAGC
TTTTCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCACCAACCAAGGGATTATAGCAAAGGCTAAGCCTGC
AGTTTACTCTGGGGGTTACAGGGAGCCGAAAGGCTTAAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTCA
TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGGG
TCAACAATGAGAGACCAGGAGTAGGTCCTATCAGTGCCCCCAGAGTAGAGAGCAATAAGAGCCCAGCCAGTGC
AGTCCCGGCTGTGTTTTCTACCTGGTGATCAGAAGTGTCTGGTTTGGCTGGCTGCCCATTTGCCCTTGTAGTGG
GCAGCCCTGGGCTTGGGCCCCCTCCCTCCGGCCCTCAGTGTTGGCTCTGCAGAAGCTCTGGGGTTCCTTCAAGT
CACGAGGGGTTAGGCTGCTGTCCCTGAGTCCCTCATTCTGTACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCC
TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCCCTGGGCTGCCCTCCCCAGACCCCTGACCACCCCTG
GGTCTGTCCCCCACCAGAGCCCCAGCTCCTGTCTGTGGGGGAGCCATCACGGTGTTCGTGCAGTCCATAGCGCT
TCTCAATGTGTGTACCCGGACCTGGGAGGGGAGGGAACACTGGGGTTTAGGACCACAACCTCAGAGGCTGCTTG
GCCCTCCCTCTGACCAGGGACATCCTGAGTTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGAGGCTTCTC
AGATTGTGGGGCACATTGTGTAGCCTGACTTCTGTGAGCTCCAGTCCAGGAGGAAAGAGCCAAGGCCACTT
TTGGGATCAGGTGCTGATCACTGGGCCCCCTACCTCAGCCCCCTTCCCTGGAGCACCTGCCCCACCTGCCCA
CAGAGAACACAGTGGTCTCCCTGTCCGGGGCGGCTTTTTCTCCTTGGAGCGTCCCTGACGGACAAGTGGAG
GCCTCTGTGTCGGGCTGCAATGGATGCAAGGGGCTGCAGAGCCAGGTGCATGTGTGATGATGGGAGGGGGCTC
CGTCTGACAGGCTGGAGGTGGCATCCACTGGACAGCAGGAGGAGGGGAGTGAGGGTAACATTTCCATTTCCCT
TCATGTTTTGTTTCTTACGTTCTTTGAGCATGCTCCTTAAACCCCAAGGCCCAATTTCCCCAAGCCCCATTT
TTTCTGTCTTATCTAATAAATCAATATTAAG

180/249

FIGURE 178

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401

><subunit 1 of 1, 370 aa, 1 stop

><MW: 40685, pI: 4.53, NX(S/T): 0

MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEPPAPQALATRALPCPAHVVFQAGREDELTITEGEWLEVIEEGDADEW
VKARNQHGEVGVFPERYLNFPDLSLPSSQSDNPGAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSSLVEELLGPPGPPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPDGKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT

181/249

FIGURE 179A

CACACGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGACAGAGACAAAGGCACAGCGGAA
GAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCAGACAGAGTCTTACAGAGGGAGAGGCCAGAGAAGCTGCAGA
AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGATTGGAGAACGACACCCCTGG
GCACCTCTCCCAAGGCCAAGGACTAAGTTTCTCCATTCTCTTAACGGCTCTCAGCCCTCTGAAAACCTTGCC
TCTGACCTTGGCAGGAGTCCAAGCCCCAGGCTACAGAGAGAGCTTTCAAAGCTAGGTTGTGGAGGACTTGGT
GCCCTAGACGGCCTCAGTCCCTCCAGCTGCAGTACCAGTGCCATGTCACAGACAGGCTCGCATCCCGGGAGGGG
CTTGGCAGGGCGCTGGCTGTGGGGAGCCCAACCCTGCCTCCTGCTCCCATTTGTGCCGCTCTCCTGGCTGGTGTG
GCTGCTTCTGCTACTGTGGCTCTCTCTGCTCCCTCAGCCCCGCTGGCCAGCCCCCTCCCCCGGGAGGAGAT
CGTGTTTCCAGAGAAGCTCAACGGCAGCGTCTGCTGCTGGCGCCCTGCCAGGTGTTGTGGCGTTGCA
GGCCTTTGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAAGTCAGGGGCTGACAGTGCAGTA
CCTGGGCCAGGCGCTGAGCTGCTGGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC
GGAGTCGGTGGCATCTCTGCAGTGGGATGGGGGAGCCCTGTTAGGCGTGTTTACAATATCGGGGGGCTGAACCTCCA
CCTCCAGCCCCCTGGAGGGAGGCCACCCCTAACTCTGCTGGGGGACCTGGGGCTCACATCTACGCCGGAAGAGTCC
TGCCAGCGGTCAAGGTCCTATGTGCAACGTCAAGGCTCCTCTTGGAAAGCCCCAGCCCCGAAGAGCCAA
GGCCTTTGCTTCACTGATAGATTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGCAATCCACGGTGC
GGGGCTAAAGCGCTACCTGCTAACAGTGTGGCAGCAGCAGCCAAGGCCTTCAAGCACCCAAGCATCCGCAATCC
TGTGAGCTTGGTGGTGAATCGGCTAGTGATCTGGGGTCAAGCGAGAGGGGCCCAAGTGGGGGCCAGTGCTGC
CCAGACCTTGGCAGCTTCTGTGCTGGCAGCGGGGCTCAACACCCCTGAGGACTCGGGCCCTGACCACCTTTGA
CAGACCCATTCTGTTTACCCTGAGGACCTGTGTGGAGTCTCCACTTGCACACGCTGGGTATGGCTGATGTGG
CACCGTCTGTGACCCGGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAGTCAGCCTTCACTGCTGCTCA
TGAAGTGGGTGATGCTTCAACATGCTCCATGACAACCTCAAGCCATGCATCAGTTTGAATGGGCTTTGAGCAC
CTCTCGCCATGTCAATGGCCCCCTGTGATGGCTCATGTGGATCTTGAAGGACCCCTGGTCCCCCTGCAAGTCCCGCTT
CATCATGACTTCTGGACAATGGTATGGGCACTGTCTCTAGACAACCAAGAGGCTCCATGCACTGCTGCTGT
GACTTTCCCTGGCAAGGACATATGATGCTGACCGCCAGTGCCAGCTGACCTTCGGGCCGAGCTACGCCATTGTCC
ACAGCTGCCGCCGCCCTGTGCTGCCCTCTGGTGTCTGGCCACCTCAATGGCCATGCCATGTGCCAGACCAAACA
CTCGCCCTGGGCCGATGGCACACCCCTGCGGGGCCGACAGGCCCTGCATGGGTGGTGCCTGCCATGGACCA
GCTCCAGGACTTCAATATCCACAGGCTGGTGGCTGGGGTCTTGGGACCATGGGTGACTGCTCTCGGACCTG
TGGGGTGGTGTCAAGTTCTCTCCCGAGACTGCACGAGGCTGTCCCCGGAATGGTGGCAAGTACTGTGAGGG
CCGCGGTACCCGCTTCCGCTCTTGCAACACTGAGGACTGCCCAACTGGCTCAGCCCTGACCTTCGCGGAGGAGCA
GTGTGCTGCCATACAACCACCGCACCGACCTCTTCAAGAGCTTCCCAGGGCCCATGGACTGGGTCTCTCGCTACAC
AGCGGTGGCCCCCAAGGACAGTGCACAACTACCTCGCAGGCCCGGCACTGGCTACTACTATGTGCTGGAGCC
ACGGTGGTAGATGGGACCCCTGTTCGCCGACAGCTCTCGGTCTGTGTCCAGGGCCGATGCATCCATGCTGG
CTGTGATCGCATATGTTGCTTCAAGAAAGAGTTTGACAAGTGCATGGTGTGCGGAGGGGACGGTTCTGGTTGCAG
CAAGCAGTCAGGCTCCTTCAGGAAATTCAGGTACGGATACAACAATGTGGTCACTATCCCCGCGGGGGCCACCCA
CATCTTGTCCGCGCAGCAGGGAACCCCTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTTA
TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCTGGGGGACATGAGTTGCGCTA
CAGCGGGGCCATCGAGCCTCAGAGACATGTACGCCATGGGCCATGGCCAGCCTTTGACACTGCAAGTCCCT
AGTGCTGGCAACCCCCAGGACACACGCCTCCGATACAGCTTCTTCGTGCCCCGGCCGACCCCTTCAACGCCAG
CCCCACTCCCCAGGACTGGCTGCACCGAAGAGCACAGATTCTGGAGATCCTTCGGCGGCGCCCTGGGCGGGGAG
GAAATTAACCTCACTATCCCGGCTGCCCTTTCTGGGCACCGGGGCCCTGGACTTAGCTGGGAGAAAGAGAGCTT
CTGTGCTGCCCTCATGTCAAGACTCAGTGGGGAGGGCTGTGGCGTGAAGCTGCCCTCCTCTGCTGCCCTAAT
GGCGAGGCTGGCCCTGCCCTGGTTTCTGCTGCCCTGGGAGGCAGTGATGGGTTAGTGGATGGAGGGGCTGACAGAC
AGCCCTCCATCTAAACTGCCCCCTCTGCCCTGCGGGTCAAGGAGGGAGGGGAAGGCAGGGAGGGCCTGGGCCC
CAGTGTATTTATTTAGTATTTATTTACTTTTATTTAGCACAGGGAAGGGGACAAGGACTAGGGTCTGGGGAA
CCTGACCCCTGACCCCTCATAGCCCTCACCCCTGGGGCTAGGAAATCAAGGGTGGTGGTATAGGTATAAGTGGT
TGTGATTCGCTGTGTGTGTGTGAAATGTGTGTGTGCTTATGTATGAGGTACAACATGTTCTGCTTTCCCTC
TTCCTGAATTTTATTTTTTGGGAAAGAAAAGTCAAGGGTAGGGTGGGCCCTCAGGGAGTGAGGGATTATCTTTT
TTTTTTTTTCTTTCTTTCTTTCTTTTTTTTTTTTGGAGACAGAATCTCGCTCTGTGCGCCAGGCTGGAGTGCAATG
GCACAATCTCGGCTCACTGCATCCTCCGCTCCCGGGTCAAGTGATTTCTCATGCTCAGCCTCCTGAGTACGCTG
GGATTACAGGCTCCTGCCACACGCCCACTAATTTTTTGTGTTTTGTTTGGAGACAGAGTCTCGCTATTGTG
ACAGGGCTGGAATGTTTCACTGCTCAGTCAACCTTCGCCACCTGGGTCCAGCAATTTCTCCTGCCTCAGCCTCC
CGAGTAGCTGAGATTATAGGCACCTACCACCACGCCCGGCTAATTTTTGTATTTTTAGTAGAGACGGGGTTTCAC
CATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTTAGGTGATCCACTCGCTTCACTCTCCCAAAGTGTGGGATT
ACAGGCGTGAGCCACCGTGCCTGGCCACGCCCACTAATTTTTGTATTTTTAGTAGAGACGGGTTTCAACATG
TGCCAGGCTGCTCTTGAACCTCCTGACCTCAGGTAACTGACCTTGTCTGCTCCCAAGTCTGGGATTACAGT
GTGAGCCACCACGCCCGGTACATATTTTTTAAATGAAATTTACTATTATGTGATCCTTTTGGAGTCAGACAG

182/249

FIGURE 179B

ATGTGGTTGCATCCTAACTCCATGTCTCTGAGCATTAGATTCTCATTGCCAATAATAATACCTCCCTTAGAAG
TTTGTGTGTGAGGATTAAATAATGTAAATAAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAAAAAAAAAA
AAGGAAA

183/249

FIGURE 180

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCILLPIVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV
FPEKLNGSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP
GTYLTTGTINGDPESVASLHWDGGALLGVLYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP
ASGQGPMCNVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA
AAKAFKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHF
DTAILFTRQDLGCVSTCDTLGMADVGTVCDFARSICAIVEDDGLQSAFTAHELGHVFNMLHD
NSKPCISLNGPLSTSRHVMAFVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PVTFFPGKDYDADRQCQLTFGPDSRHCPQLPPPCAALWC SGHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCLHMDQLQDFNIPQAGGWGPWGDSCSRTCGGGVQFSSRDCTRVPVRNGGKY
CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVAPQDQCK
LTCQARALGYVYVLEPRVVDGTPCSPDSSSVQVGRCIHAGCDRIIGSKKKFDKCMVCGGDG
SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL
MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
PSTPRPTPDWLHRRQAQILEILRRRPWAGRK

Important features of the protein:**Signal peptide:**

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGG
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC
AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTTTGGTATCCTGGCCCTAACTCT
AATTGTCTGTTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA
TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTG
ACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT
TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA
TTAAAGTGATTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
ACAACCTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
TTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC
CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT
CCTGCCAACGAAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT
AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTG
AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT
CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA
CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCC
GCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATAT
AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCT
CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC
AAAAAAAAAAAAAAAAAAAA

185/249

FIGURE 182

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIIYFVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKN SKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPLDERGYCCIIYCRGRNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWV
ARMLGRV

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-
242**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

186/249

FIGURE 183

GCGGAAGTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCC
CGGCTGGCCTAGGCAGGCAGCCGCACC**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT
GCTCAGCTTCTTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA
CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAG
TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
CCAAGACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT
GCGCCTGCGCCGTATCGGGATGAAGTGACGCGCTGCGCCAAGGGCACACCCGCCAAGACC
ACCTTTGCCATCCTCGGCGGCACCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT
CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGA
AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
GGCACCTGCTTTGCCTGTCTCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCGCC
CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG
ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC
AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATA
ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA
AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATAT
TTATGTGGGTGATTTGATAACAAGTTTAAATATAAAGTGAAGTTGGGAGTTTGGTCAGTGGGGT
TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

187/249

FIGURE 184

MASTAVQLLGFLLSFLGMVGTLITTILPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTL
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQ
DEAPYRPHYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

FIGURE 185

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG
CAGGCGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACCACATGCCAAGTGGTGGCGTTCTCT
CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC
AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC
CATGCTGCAGGCAGTGCGAGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCC
TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
AACATGACACTGACCTCCGGGATCATGTTTATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT
GTCTGTGTTTGGCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG
GCATGGGTGGGATGGTGCAGACTGTTTACAGACCAGGTACACATTTGGTGCGGCTCTGTTTCGTG
GGCTGGGTGCGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG
CCTGGCACCAGAAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTG
CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAG
ATATACGATGGAGGTGCCCCGACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA
TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAA
AACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGGTCTCACAGCTGGAAGTTAGAAAAGC
CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC
ACCATAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT
TTCTTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC
ATTTTGATGATTTAGACAGACTCCCCCTCTTCCTCCTAGTCAATAAACCCATTGATGATCTA
TTTCCCAGCTTATCCCCAAGAAAACCTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT
CTGCTGTTTGAATTTTGTCTCCCCACCCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA
GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG
TGATCTTAAAAGTTACCAAACCAAAGTCATTTTTCAGTTTGGAGCAACCAAACCTTTCTACTG
CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCCTGAGCTCTCCACTGGAG
TCCTCTTTCTGTGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAAT
TTAAGTCCTAAATATAGTTAAAATAAATAATGTTTTAGTAAAATGATACACTATCTCTGTGA
AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAAATAATTGCTTTGACATTGTCT
ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC
CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCTG
GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG
GCATACACCTGTAGTCCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG
AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA
TCCTGTCTAAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAA

189/249

FIGURE 186

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCG
GAGTCCAGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTG
GGCTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG
AGAGTGTGGCCTTCATTGAAAACAACATCGTGGTTTTTTGAAAACCTCTGGGAAGGACTGTG
GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG
CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC
TTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA
GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC
TCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
GTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCT
GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA
GATACTCGATACCTTCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCG
AGCGTCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGC
CATGCAATGACAAAAATCTATATTACTTTCTCAAATGGACCCCAAAGAACTTTGATTTA
CTGTTCTTAACTGCCTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAA
GCTATTTTACGCAGAATGAGATATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT
TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTATCATTTACTTCAAATGACATTGCT
AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG
TGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAAATGAAATGCCAG
TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTG
AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCTCCATTTATAATGA
AGATTAAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTG
TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTT
TTCTTGTGTATTAAATTAACATTTTTTAAACGCAGATATTTGTCAAGGGGCTTTGCATTCA
AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
GTTTTAGGAAAGTGAAAATATTTTTGTTTTGTATTTGAAGAAGAATGATGCATTTTGACAA
GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
AATATAAATAAAAGAGCAGAAAAATATGTCTTGGTTTTCATTTGCTTACCAAAAAACAACA
ACAAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTG
TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTGTACCATTTCTGTTTAGTTTTACTAAA
ATCTGTAAATACTGTATTTTTCTGTTTATCCAAATTTGATGAACTGACAATCCAATTTGA
AAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATA
TTAATAAATTGTACATTTTTCTAATT

191/249

FIGURE 188

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

192/249

FIGURE 189

TCGCCATGGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGGCTGGGTG
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
CGTGGTGGCCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
GCCCTCTGTGTCATCGCCCTCCTTGTGGCCCTGTTGCGCTTGCTGGTCTACCTTGCTGGGGC
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCCGCCTGGTGTCTACCTCTGGGA
TTGTCTTTGTCTCTCAGGGGTCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC
ATCCGGGACTTCTATAACCCCCCTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCCTCCCT
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGCTGGGTGGGGGGTTGCTGTGCTGCACTT
GCCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCCCT
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCTGACGTGGAGGGGAATG
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT
CGTACCTTTTGTCTCTGCCTCCTGCTATTTTTCTTTTACTGAGGATATTTAAAATTCATTT
GAAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCTTGG
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC
CAGTCAAGCTATGGAACATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC
TGTCCCCAAGAGTTCCTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTCACCCCTGGAAAAACAAATCATCTG
TTAACAAAGGACTGCCCACCTCCGGAACCTCTGACCTCTGTTTCCTCCGTCTGATAAGACG
TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
CTTCTGCCCTGCCCCCCTCGTCTCACCCCTTTACTCTCACATTTTTATCAAATAAAGCATG
TTTTGTTAGTGCA

193/249

FIGURE 190

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGWMSCVVQSTGQM
QCKVYDSLALPQDLQAARALCVIALLVALLFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLPVCWTAHAIRDFYNPLVAEAQKRELGLSLYLGWAASGLLLLGGGLLCCTCP
SGGSQGPHSHMARYSTSAPAISRGPSSEYPTKNYV
```

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG
AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATTATTTATCCC
TTGCAAATTGCTGGGCTGGTTCTTGGGTTCCCTTGGCATGGTGGGGACTCTTGCCACAACCCT
TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGGAGCAACATTATTGTCTTTGAGAGGCTC
TGGAAGGGCTCTGGATGAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
TAGCTCCTTGTTGGCTCTCCCGCCTGCCCTGGAAACAGCCCCGGGCCCTCATGTGTGTGGCTG
TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
GGCTCTAACGAGAGGGCCAAAGCATAACCTTCTGGGAACCTCAGGAGTCCTCTTCATCCTGAC
GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA
ACCCAGCCATCCACATAGGTCAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA
AGCGCTGCTGTCCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGCTGCTGCAACAGAAA
GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA
ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTTGGCTCCAAGT
ATGGACTATGGTCAATGTTTTTTATAAAGTCCTGCTAGAACTGTAAGTATGTGAGGCAGGA
GAACTTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG
AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG
GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG
TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA
GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

195/249

FIGURE 192

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRD FYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV

Important features of the protein:

Transmembrane domains:

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAAGATCACTGGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA
CATACTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTAAATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG
AGTTTCTTTCAGTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTG
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
TTTTTTTTTAAACACGTCAATAAAAAAATAATCTCCCAGA

197/249

FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN

ECHLCTESLKSNQGRVQFLHDGSC

Signal peptide:

amino acids 1-19

FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCCCTCGCCCTCCTGCTCGCGCCC
CGCCGCCATGGCTGCCTCCCCCGCGCGGCCTGCTGTCCTGGCCCTGACCGGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAA
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA
ATTCCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCGAGGTGC
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG
TCAACTACGATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATT
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTACGCAGAT
CTTTTCTACCTACTTTGTGTGATCAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTT
TGATATTTTCATGGGAATGCCTCTCATTTAAAATAGAAATAAAGCATTTTGTTAAAAAGA

199/249

FIGURE 196

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKCLKMLQKREAPVPTKTKVAVDENKAKEFL

GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDYYQRHYD

EDSAIGPRSPYGFRHGASVNYDDY

Signal peptide:

amino acids 1-30

200/249

FIGURE 197

CGGCTCGAGCCCGCCCGGAAGTGCCCGAGGGGCGCGATGGAGCTGGGGGAGCCGGGCGCTC
GGTAGCGCGGCGGGCAAGGCAGGCGCCATGACCCTGATTGAAGGGGTGGGTGATGAGGTGAC
CGTCCTTTTCTCGGTGCTTGCCTGCCTTCTGGTGCTGGCCCTTGCCTGGGTCTCAACGCACA
CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTAGGGACCCCAACGCCATCCCAGCCCAGC
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCCAGCACGGGGTTTACAGCAACACCGCCAG
CCCCGGACTCCCCGCAGGAGCCCCTCGTGCTACGGCTGAAATTCTCTCAATGATTCAGAGCAG
GTGGCCAGGGCCTGGCCCCACGACACCATTTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCTTGG
GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
CCAAATCCCCCCTGCCCCGCCGGGGTCCGAGCCCCGGCCCCCTCCGGGCTGGAAATCGGCAGCCT
GCTGCTGCCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
CCTTCTTTCCCCTGACCGCCACTCTGGGCCTGGCCGGCTTCACCCTGCTCCTCAGTCTCCTG
GCCTTTGCCATGTACCGCCCGTAGTGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCCCTCC
GGACCTTGCTCCCCGCGCCGCGGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG
CCTCTTCCCCTGCCCTGGAGCCCAGCCCTGCGCCGCAGAGGACTCCCGGGACTGGCGGAGG
CCCCGCCCTGCGACCGCCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA
CTGGGAGTGGGCTCCTCGGGGTGCGGCATCTGCTGTGCTGCCTCGGCCCCGGGCAGAGCCG
GGCCGCCCCGGGGGCCGTCTTAGTGTTCTGCCGAGGACCCAGCCGCCTCCAATCCCTGAC
AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTCGGTGGGAGGCTGGTGAAGGGGAGCGGGGAG
GGGCAGAGGAGTTCCCCGAACCCGTGCAGATTAAAGTAACGTGAAGTTTTAAAAAAAAAA
AAAAAAA

FIGURE 198

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRRLKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

202/249

FIGURE 199

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATCCCCCAGGCTCTCAGAGAAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCC
TCAGCTGCACCTCCTCCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTTGGTCAGCAGC
TTTCTTGGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT
GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG
AAAGCAAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTC
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCA
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGACAGGCATCCACTGCGCAAAAAGGA
TTGTGTCCGGAGCACGGGGGATGAACAACCTGGGTAGAATGGAGGTTGCACTGTTTCAGGCCGG
CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGATGAAACAGGGTGCGGGTGCACCGTGG
AGTCATTCCAAGACTCCTGTCTCACTCAGGGATTCTTCATTTCTTCTTCTACTGCCTCCA
CTTCATGTTATTTTCTTCCCTTCCCATTTACAACATAAACTGACCAGAGCCCCAGGAATAAA
TGGTTTTTCTTGGCTTCCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTAT
TTGTAAACTGAGGACCACAATAAAGAAATCTTTATATTTATCG

FIGURE 200

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI

NENADGSFDYGLFQINSHYWCNDYKSYSENLCNVDCQDLLNPNNLAGIHCAKRIVSGARGMN

NWVEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCA
CCAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGAAAGAAACACCTGAG
CAGAATGGAATCATTATTTTTTTCCCAAGGAGAAAACCGGGTAAAGGGAGGGAAGCAATTC
AATTTGAAGTCCCTGTGAATGGGCTTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC
TTGGGGTGAAACTTGGGTCCTGTGGTTTTCTGATTGTAAGTGGAAGCAGGTCTTGACACGCG
TGTTGGCAAATGTCAGGACCAGGTTAAGTGACTGGCAGAAAACTTCCAGGTGGAACAAGCA
ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC
CTGTTGCATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATG
CAGACTCCAGTTCCTCCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGT
TGCACCCTCCCCACCACACCCTGCACCAGACTGTCACAGCCCAAGCCAGCAAGCACAGCCCT
GAAGCCAGGTACCGCCTGGACTTTGGGGAATCCCAGGATTGGGTACTGGAAGCTGAGGATGA
GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTCACTGCGGGAGGATCAGC
TGCTGGTGGCCGTGGCCTTACCCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGG
AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGGACTGGGG
GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTACGCCCTGGACCCAC
GTGGCCTCCAGGAGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGG
CACCCACTGTGTCTGCAGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG
TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC
CCAGGGCCTTCCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTCAAG
TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG
GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT
TCATGGATGCCCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCCCTCCTCAGCAGAATAGCT
GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA
TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTTCCACTGGGAAC
CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTG
GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC
TCTTATGTGCTGCGAGGTGGTGAAAACCTCGAACTGTCTTTCAAGGCCTGGCTCTGTGGTG
GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAATCAGGATTCCCAT
TCCCCCTCGACCAGGAGGCCACCCTGAGGAACAGGGTTCGCATTGCTGAGACCTGGCTGGG
GTCATTCAAAGAAACCTTCTACAAGCATAGCCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGA
AGCCAGACTGCATGGAACGCTTGCAAGCTGCAAAGGAGACTGGGTTGTGCGGACATTCCACTGG
TTTCTGGCTAATGTCTACCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGAAA
GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAGGGGACATCCTGGGCT
GTCCCATGGTGTGGCTCCTTGCAGTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC
AGGAAGGAGATTCACTTTGGCAGCCCACAGCACCTGTGCTTTGCTGTGAGGCAGGAGCAGGT
GATTCTTCAGAACTGCACGGAGGAAGGCCCTGGCCATCCACCAGCAGCACTGGGACTTCCAGG
AGAATGGGATGATTGTCCACATTCTTTCTGGGAAATGCATGGAAGCTGTGGTGCAAGAAAAC
AATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAGCCCGCCAGCAGTGGCGATTTGACCA
GATAAATGCTGTGGATGAACGATGAATGTCAATGTGCAAGGAAAAGAGAATTTTGGCCATC
AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTCATGAAGCTGATCCTTTTGTGT
GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAAGAATATAGGAAGTTTCTCCTTT
TCACACCTTATTTCAATTGACTGCTGGCTGCTTA

205/249

FIGURE 202

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQT VTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGE EYS PLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR
RQDKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDL SQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP
VIDVIDWKTFQYYPSKDLQRGVLDWKLDHFWEPLPEHVRKALQSPISPISPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGH IYQNQDSHSPLDQEATL
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEKPDCMERLQLQRR LGCRTFWHFLANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP
QHLCFAVRQEQVILQNCTEEGLAIHQQHWDFQENGMIVHILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACACAGCTGAGGAAGACCTCAGACATGGA
GTCCAGGATGTGGCCTGCGCTGCTGCTGTCCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC
TGCCCCCTCCCACCGCCTGCTCAGGGCTCTTCATCCTCCCCTCGAACCCACAGCCCCAGCC
CGCCCCCGTGTGCCAGGGGAGGCCCCCTCGGCCCCACGTCTGTGTGCGTGTGGGAGCGAGC
ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTGCGGAAGTCTGCCTGGCACTG
CACCCCCAGCCACCCCATCAGGCTTTGAGGAGGGGCGCCCTCATCCCAATACCCCTGGGCT
ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG
ATTTCTGGACTATGGTTTTGTCAGCCCCCTCATGGGCTCGCAACCCACACCCCAACTCAGACT
CCATGCGAGGTGATGGAGATGGGCTTATCCTTGAGAGGCACCTGCCACCCTGCGGCCATTCT
CTGTTGCGGGGCGGTGGGGAAGGTGTGGACCCCCAGCTCTATGTCACAATTACCATCTCCAT
CATCATTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC
GACGCAGACCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGAGCCAGCAGCCACTGACA
GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCTTCGGGGACTCACCTACCCCCACCCC
TGACCATGAGGAGCCCCGAGGGGGACCCGGCCTGGGATGCCCCACCCCAAGGGGGCTCCAG
CCTTCCAGTTGAACCGGTGAGGGGAGGGGCAATGGGATGGGAGGGCAAAGAGGGAAGGCAAC
TTAGGTCTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGGTAGTGAGGAGGCAGGCGTGGC
CTCCACAGCCCCCTGGCCCTCCCAAGGGGGCTGGACCAGCTCCTCTCTGGGAGGCACCTTC
CTTCTCCCAGTCTCTCAGGATCTGTGTCCTATTCTCTGCTGCCCATAACTCCAACCTCTGCCC
TCTTTGGTTTTTTTCTCATGCCACCTTGTCTAAGACAACCTCTGCCCTCTTAACCTTGATTCCC
CCTCTTTGTCTTGAACCTTCCCCTTCTATTCTGGCCTACCCCTTGTTTCCTGACTGTGCCCTT
TCCCCTTCTCTCAGGATTTCCCCTGGTGAATCTGTGATGCCCCAATGTTGGGGTGCAGCC
AAGCAGGAGGCCAAGGGGCGGACAGCCCCCATCCACTGAGGGTGGGGCAGCTGTGGGGA
GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCTTGCACACCACCCGGAACACTCCCCAGCC
CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCTCACATATCTGTGACTTCG
GGTCCCTGTCCCCACCCCTTGTGCACTCACATGAAAGCCTTGCACACTCACCTCCACCTTCAC
AGGCCATTTGCACACGCTCCTGCACCCTCTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT
CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCCACATTCTGTGCTCAGCTCACTCAG
TGGTCAGCGTTTCTGACACTTTACCTCTCATGTGCGTTTCCCGGCTGATGTTGTGGTGG
TGTGCGGCGTGTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGCAGCCCCCTGC
GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGGCCCTCATCGGTATGG
TCTCGTCCCATTCCACACCATTTGTTTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA
TCACCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCCAGCCCA
CTGCTAAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCCTGCTGCACTACATGAGAA
AGGGACTCCCATTGTGCCCTTCCCTTTCTCTACAGTCCCTTTTGTCTTGTCTGTCTGGCTG
TCTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCCTCCCTTCCCAGCCT
CCCTTTGGGCCCTCCCTAACTCCACCTAGGCTGCCAGGGACCGGAGTCAGCTGGTTCAAGGCC
ATCGGGAGCTCTGCCTCCAAGTCTACCTTCCCTTCCCGGACTCCCTCCTGTCCCTCCTTT
CCTCCCTCCTTCCCTTCCACTCTCCTTCCCTTTTGCTTCCCTGCCCTTTCCCCCTCCTCAGGTT
CTTCCCTCCTTCTCACTGGTTTTTCCACCTTCCCTTCCCTTCTTCCCTGGCTCCTAGGCT
GTGATATATATTTTTGTATTATCTCTTCTTCTTGTGGTGATCATCTTGAATTACTGTG
GGATGTAAGTTTCAAATTTTCAAATAAAGCCTTTGCAAGATAA

FIGURE 204

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKEGEGECLRESFEESWTPNYKQCSWSSLNYGIDLKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGGLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

208/249

FIGURE 205

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGATGG
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC
CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACC GCGCAGGAGCGGCTGGACCAGGGC
GGCGGGTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
CGTGGTGCTGGCGCTCGTGGTCGTCGCGCTGAGAAAGTTTTCTGCCTCCTGAAGCGAATAAA
GGGGCCGCGCCCGGCCGCGCGCGACTCGGCAAAAAAAAAAAAAA

209/249

FIGURE 206

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVVESTSPGREPVDTG
PPAPTVAAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

210/249

FIGURE 207

GGCCGTTGGTTGGTGC GCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGG
CGGGCCGGGACGGGC **ATG**GCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA
CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
ACTTCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTCAGGGGCGCTGCTCACCGACTGGAGC
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA
CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC
CCGGGTATTTCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCC **TAAG**TAGCCC
CCAGAGGCGCTGGGAGTGTTGCCACCGCCCTCCCCTGAAGTTTGCTCCATCTCACGCTGGGG
GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCAT
CGACTGTCAGCACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACCTGCACAG
ACTCGCACGTCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT
GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGAGGGGGCTCCCCGCCTTCCAC
CTGGCTGTCATCGGGTAGGGCGGGGCCGTGGGTTCAGGGGCGCACCACTTCCAAGCCTGTGT
CCCACAGGTCCTCGGCGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACTACATAAATAAC
TGGCACAAGTAAGTCCCCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG
GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCCACGTCCTAGAGGGGCTCCCGA
GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAG
GTCTCCGACCCTCAGCTGGAGGCGGGCATCTTTCCTAAAGGGTCCCCATAGGGTCTGGTTCC
ACCCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC
ATGGAGGGGCTGACTGCCCCACATTGCCTTTCAGACAGGACACGAGCATGAGGTAAGGCCGC
CCTGACCTGGACTTCAGGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCT
AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC
CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG
CCTGGGACACACAGAGCCACCCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA
AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGGCCTGCACACCCTTCGGACATCCCAGGC
ACGAGGGTGTCGTGGATGTGGCCACACATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCT
GGGGCCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
CCGCAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCCACACTTGGCCAACCTGACCT
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC
GTGGGGGCGGAGACTCAGCTGGACAGCCCCCTGCCTGTCACTCTGGAGCTGGGCTGCTGCTGC
CTCAGGACCCCTCTCCGACCCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG
GAGGGAATGGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGCAGAGCTGCGGGA

211/249

FIGURE 208

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK

ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIER

HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDL P

Signal peptide:

amino acids 1-15

FIGURE 209

AGCAGGAGCAGGAGAGGGACAATGGGAAGCTGCCCCGTCCAGGTTTCATGTTTCCTCTTATTTCT
CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG
GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTCATTGCTGCC
ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAAATACCAGCAGTGCCCATACTCCA
TAGCATGGTGC AAAAATTTCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGA
CACACTACAACATCACTGGGAACACCATCTGCCTCTTTTCGCCTGGTAGACAATGAACAACCTG
AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTTCATTGAGAT
CAACAGCCTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCG
TAATTCAGATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG
CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG
TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTCAAACCTAAAGGAGTCTCAACTGCCAG
CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAGTTTCC
GTAGAGCATGTGCAAACTTTTGTGATGGATTCTTAAGTGGAATAATTGTTGAAAGAAAATCG
TGAATCAGAAGGAAAGACTCCAAAGGTGGAACCTCTGACTTCTCCTTGGAACCTACATATGGCC
AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG
GATCACTAGGCCTGCCAACCACACACACACGACGTGCACACACGCACGCACGCGTGCACAC
ACACACGCGCACACACACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTC
TTCTTCCTTCTTTTAAATTTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT
CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
CCTCTATGAAAGAGAGGCATTCTTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT
TTGTATACTGCACATGACTTACACACAACATAGTTCTGCTCTTTTAAGGTTACCTAAGGGT
TGAAACTCTACCTTCTTTCATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGG
ATGGTTTTTAACACCTTTGTGAAATTGTCTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
CCTGAACTCAGCAGAAATAGACCATGTGAAACTCCATGCTTGGTTAGCATCTCCAACCTCCC
TATGTAAATCAACAACCTGCATAATAATAAAAGGCAATCATGTTATA

213/249

FIGURE 210

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPGAAQEPTWLTDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPVSGFISTDSEVLTHYNITGNTICLFRLLVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA
KLFQGGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTG
GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGGAGCCGGG
GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTTCGGTCTGGCGGCGGCGCTTGG
GCTCTTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA
ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCGTTTTTCCACTACTC
CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTTAAAGACAGAATCAGCTGGGCTGGAG
ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC
TATATCTGTGATGTCAAAAACCCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA
TGTCGTAGAAAAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
CTGTGGTCTTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCTCTATAGAAGGAAA
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTCAACAGTTAAGCAGGC
TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC
AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAAC
AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAATTAAGAGAATACCTAGAACATATC
CTCAGCAAGAAACAAAACCAAACCTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT
AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA
TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTC
AGGTCATTTACAATTGGGAGATTTTCAAGAACATTCCTTTTACCATCATTTAGAAATGGTTTG
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG
GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAA
AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT
AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTG
AAATGTGTCATATCAATTTCTGGATTCATAATAGCAAGATTAGCAAAGGATAAATGCCGAAG
GTCACCTTCACTTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAATCCAAGCTTTGCTT
GAGAACTTTTGTAACGTGGAGAGTAAAAAGTATCGGTTTTTA

215/249

FIGURE 212

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKKDASINIEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTGCGSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSDKINKSESVYADIRKN

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

216/249

FIGURE 213

GCCGGCTGTGCAGAGACGCC**ATGT**ACCGGCTCCTGTCAGCAGTGACTGCCCGGGCTGCCGCC
CCCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC
TCTCGGCCACGGCTGGGTCTGGGGGCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC
TGGCAGGTGGGCTGAGGGGCGCGGCCCCGGCGCAGTCCCCCGCGGCCCCGACCCTGAGGCG
TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCCGGC
GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAAGTC
TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT
TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG
CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCAGAAAAAGAA
TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGGAATTCG
TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA
TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAAGGCCAAAGTAATGAAAAGAATGATTTT
ACTAAATTTAAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAACCTGGCAAGAA
AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTCAATTGAAT
CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA
ACTTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA
CTATATGCAGAAAATATTCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
CAGTGATTTACAATAGAGCAAGG**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC
TTAACACTATTTTATTAATTAAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC
CACATTTTGGGAGCTTTTCTACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAAACA
TGTTTATAAAGTAAAAAAA

217/249

FIGURE 214

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGGLGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCPETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRAR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG
AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC
TCTTGCTGATGGCGGTAGCAGCGCCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCCGGGACT
GGTGC GCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT
GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT
GGAAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC
CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG
GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG
TGGAGTCGCACCTGTCCGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC
GTGTCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA
GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCCACCACAGCCCCAGGCCCTGAGACGGCGG
CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG
TCCTTCCTCGCCAAATACTGGATGTACATCATTCCTCGTCCTGTTCTCATGATGTCAGG
AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC
TTTGCTGTGTGCCACCCTCCCTGTAAGTCTATTTAAAAACATCGACGATACATTGAAATGTG
TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG
TCCTGATGTACAAGCTTGATTGAAATTCAGTCTCACTTGATACGTTATTCAGAAACCCAAG
GAATGGCTGTCCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT
TAAACTGTCCCCCAGATCGACACGCAAAAAAAAAA

219/249

FIGURE 216

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGLRDVAALNGLYRVRI PRRP GALDGLEA
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETA AFIERLEMEQAQKAKNPQEQKSFFAKYWMIIPVVLFLMMSGAPDTGGQ
GGGGGGGGGGGSGLC CVPPSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT
GGAGCCGGACGTGTCCGGGGCGTCCCCGCAGACCGGGGCAGCAGGTGTCGGGGGGCCCACC
ATGCTGGTGA CTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGA ACT
GTCAAGATGCCGGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTTCGGTTTC
AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
CTCTATAAACTCTACCA GCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
TGGCCTTGCCCTCTACAGTCCTCTTTGGCCTAGTGGCCTCCTCCCTTGTTGGATTGGCTGGGTC
GCAAGAATTCTTGTGTCCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAA ACTCTCT
CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT
CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT
GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC
CATCCCTCTCCTGGCTCTGGCAGGGGCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC
GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTGCGACCGCCGC
GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGT CATCTTCATCTTTGTCTTCCT
CTGGACACCTGTGCTGGACCCACACGGGGCCCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG
CCCATGCACCTGCTGTCCCTGCTGTGCTCATCGTCGTCTTCTCTCTCTTCATGTTGACTTT
CTCTACCAGCCCAGGCCAGGAGTCCGGTGGAGTCCTTCATAGCCTTTCTACTTATTGAGT
TGGCTTGTGGATTATACTTTCCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA
GAGCAGGCTGGTGTACTCAACTGGTTCCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT
CCTTGTCCTCCATGACAGTGATCGAAAAACAGGCACCTCGGAATATGTT CAGCATTTGCTCTG
CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTACCGTG GTAAGGCATGATGCT
GAGCTGCGGGTACCTTACCTACTGAGGAGCCCTATGCCCCTGAGCTG**TAA**CCCCACTCCAG
GACAAGATAGCTGGGACAGACTCTTGAATTCCAGCTATCCGGGATTGTACAGATCTCTCTGT
GACTGACTTTTGTGACTGTCCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA
TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTCCCTCTGTGTTACTCCCATTTAGAAA
ATAAACACTTTTAAATGATCAAAAAAAAAA

221/249

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFNNHVLAVVAG
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAF'SRTCAGGLRCLLSDRR
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGII FSSFMAASLLGSSLYRIATSKRYHLQ
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPET
EQAGVLNWFRVPLHSLACLGLLVLHDSRKTGTRNMFSCSAVMVMALLAVVGLFTTVVRHDA
ELRVPSPTTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
314-330, 343-359, 379-394, 410-430

222/249

FIGURE 219

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAGATG
GTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTGC GCGGCCCA
CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTGATACA
TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
CACCTTGTCGCCCGCTGAACCTCCAGAGGCCTGCGGGGAACTCAGCAACGGTTTCTTCATCCA
GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCC
AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGG
CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT
CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
TGGTAGAAAGAGTTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA
AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG
GCCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT
CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
AGTGGTTTAAAGAGCTGGTGTGTTGGGGACTCAATAAACCCCTCACTGACTTTTTAGCAATAAA
GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 220

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

Signal peptide:

amino acids 1-20

FIGURE 221

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGTGA
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG
ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG
AGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACC
TGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCATAACATTGTATGGAT
TTATCTCAACGCTATTGTTTAATGGCTGTGTTTAATGTGATCTATCTGGAAAATGAGGACTC
CGAATAAAAAGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

225/249

FIGURE 222

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538

><subunit 1 of 1, 116 aa, 1 stop

><MW: 12910, pI: 6.41, NX(S/T): 1

MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCgiYKDNNKSSiHCMDLSQRYCLMAVFNViyLENEDESE**Important features of the protein:****Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTTCCTTCTGGATGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAG
GGTGCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTTACAGCACCACTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAACTTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCCAGCCAAG
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC
AGCAAACCTACCCCGTGGGTGCGC**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAA

227/249

FIGURE 224

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541

><subunit 1 of 1, 178 aa, 1 stop

><MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK

LGDSWDVKLGALGGNTQEVTLQPGYITKVFVAFQAFLRGMVMYTSKDRYFYFGKLDGQISS

AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

Signal peptide:

amino acids 1-22

FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT
GAACTGGGTGCTCATCACGGGAAGTCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
CCCCAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTT
TTTTTTTTTAACCGCCCCCTCCCCACCCCCCAAAAAAAGTAAAGATGCAAAAACGTAATAT
CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT
TATTTGTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT
CCCAAGGGGTCCAATTTTTCTTCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTG
ACAGGGGCTGTCATGCAACTGGCCCCAAGCCAAAGCAAAAAGACCTAAGGACGACCTTTGAA
CAATACAAAGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
ATAGCCCCACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG
TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA
TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAACCTTAAGTATAAT
CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT
TGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA
TCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATTTACGGAAGCTGGATCTGTCC
TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTTCGGGGCTTGCGGAAGCTGCTGAGTTT
ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC
TGGAAGCTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC
ATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCT
TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAATAAAATCAGTGTCTATAG
GACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATC
GAAGCTTTTCACTGGACCCAGTGTTTTCCAGTGCTGCCGAATCTGCAGCGCCTCAACCTGGA
TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA
TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAAGCTGGCTG
AAAAGTTTTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG
AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAGTACTACAGAGAGGT
TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCAT
GAGAGCAAACCCCTTTGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC
TGACGCCGAGCACATCTCTTTCCATAAAATCATCGCGGGCAGCGTGCGCTTTTCCTGTCCG
TGCTCGTCATCCTGCTGGTTATCTACGTGTCATGGAAGCGGTACCCTGCGAGCATGAAGCAG
CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAAT
GACTCCCAGCACCCAGGAATTTTATGTAGATTATAAACCCACCAACACGGAGACCAGCGAGA
TGCTGCTGAATGGGACGGGACCCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAAGAGCTCTTAAAAGCTGGGAAATAAGTGGTGCTTTATTGAACTC
TGGTGACTATCAAGGGAACGCGATGCCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTG
CAAGATCCTTCCCTGTCCGTTTTAGTGCATTATAACTGGTCATTTTCCCTCTCATACATA
ATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTTGAAGCTCCGGTTAATATAA
TACCTATTGTATAAGACCCTTTACTGATTCCATTAATGTGCGATTTGTTTTAAGATAAACT
TCTTTCATAGGTAAAAA

229/249

FIGURE 226

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPT VLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRI FQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKEHLEHNQFSKLNALFPRLVSLQNLYLQWNKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIGQEILDSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT
TAAATATGTCAAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG
TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG
TGGCAGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA
ATTGATTCTCACAGGCGCACCATGGCAGTTTTTGGCTGTTGGAGACTTGGACTCTATTTATGG
GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT
ATCCTGTTCCCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
AAAACAACCTTGATTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA
AAACATCAAATTTAGGAATAGTTATTTAGTTGTTGGAAATGTCCAGAGATCTATTCATATA
GTCTGAGGAAGGACAAATTCGACAAAAGAATGGATGTTGGAAAAAATTTGGTCATGGAGATG
TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC
AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC
CTAGCATGGGGTCCATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT
GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
CAGCAAAAACAAGAGGTTTTATGCCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC
CTTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTG
GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC
AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA
CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT
AAACATCAATAGATATCTAAAAA

231/249

FIGURE 228

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCEEDEMVCVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGCGGAGTAAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT
TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTA
GCTCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGCGGCGACCGTGACGAGAAGCCC
ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAAGTCAGATGCCCTTTTAAACT
CCCTCTTCAAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG
ATGAAGAATATACAATATTGAGGATATTTTTTTCTTTTTTTTTTCAAGTCTTGATTTGTGGC
TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGTTGCTTCTTCAGAAATGTTTTTA
CAATCTCAAGAAAAAATATGTCCCAGAAATGAGTTTACTGTTGCTTGATTTGGACTCATT
TGGGGATTGATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA
ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATT
GCTGTCCTTCTGGATGACATTTTGAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
TGTTGTGAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA
CCACAAATAAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAAATCACCTTGTC
TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC
AGAGCAATACTTTACAATAAAAGCTCTACACATTTTTCAAGGAGTATGCTGGATTTCATGGAAC
TCTAATTCTGTACATAAAAATTTTAAAGTTATTTGTTTGCTTTCAGGCAAGTCTGTTCAATG
CTGTACTATGTCCTTAAAGAGAATTTGGTAACTTGTTGATGTGGTAAGCAGATAGGTGAGT
TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTC
ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTTGACAAGTGAAGAATGTTTAA
TCATTCGTGCATTTGTTCTCAATAGATGTAAGTGTAGACTACGGCTATTTGAAAAAATGTG
CTTATTGTACTATATTTTGTATTCCAAATTATGAGCAGAGAAAAGGAAATATAATGTTGAAAA
TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGA
AGGTTAATTATTGTATATTTTAAAAATTACACTTATAAGAGTATAATCCTTGAAATGGGTAG
CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAATAGTT
GTAACTCTAATCTTATACTTATTGAAGAATAAAAGATATTTTTTATGATGAGAGTAACAATA
AAGTATTCATGATTTTTTACATACATGAATGTTTCAATTTAAAAGTTTAAATCCTTTGAGTGTCT
ATGCTATCAGGAAAGCACATTATTTCCATATTTGGGTAAATTTTGCTTTTATTATATTGGTC
TAGGAGGAAGGGACTTTGGAGAATGGAACCTTTGAGGACTTTAGCCAGGTGTATATAATAAA
GGTACTTTTGTGCTGCATTAAATTGCTTGGAAAGTGTTAACATTATATTATATAAGAGTATC
CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC
TTAAAATAAGAACATTTAAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAAGCT
GTATATAGCACAGGGAACCCTAATCTTGGGTAATTCTAGTATAAAACAAATTATACTTTTAT
TTAAATTTCCCTTGTAGCAAATCTAATTGCCACATGGTGCCCTATATTTCATAGTATTTATT
CTCTATAGTAACCTGCTTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAATTTAGATAT
TGTATTGTTTCGTCAATTATAATATGCTACCACATGTAGCAATAATTACAATATTTTATTAAAA
TAAATATGTGAATATTGTTTCATGAAAGACAGATTTCCAAATCTCTCTTCTCTCTCTGTA
CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

233/249

FIGURE 230

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648

><subunit 1 of 1, 140 aa, 1 stop

><MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR

Important features of the protein:**Signal peptide:**

amino acids 1-26

FIGURE 231

CGCGGCCGGGCGCCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC
CATGCCGTGGCCCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCAGACAACCCGGCCATGCT
TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCCTGACTCGG
GTGGATTGTAGCGGCCTGGGCCCCCACATCATGCCGGTGCCCATCCCTCTGGACACAGCCCA
CTTGACCTGTCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGGCGGGGCT
ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCCTGCTGCC
TTCTCCCGCCTTCGCTACCTGAGTCGCTGACCTCAGCCACAATGGCCTGACAGCCCTGCC
AGCCGAGAGCTTCACCAGCTCACCCTGAGCGACGTGAACCTTAGCCACAACCAGCTCCGGG
AGGTCTCAGTGTCTGCCTTCACGACGCACAGTCAGGGCGGGCACTACACGTGGACCTCTCC
CACAACCTCATTCACCGCCTCGTGCCCCACCCACGAGGGCCGGCCTGCCTGCGCCCAACAT
TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGCCCC
TGCGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCATTGGTCCGGGTGCCTTCGCGGGG
CTGGGAGGCCTTACACACCTGTCTTGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG
TGGCTTCCGTGAGCTACCGGGCCTGCAGGTCTGGACCTGTCGGGCAACCCCAAGCTTAACT
GGGCAGGAGCTGAGGTGTTTTAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTTCGGGCACC
AACCTGGTGCCCTGCCTGAGGCGCTGCTCCTCCACCTCCCGGCACTGCAGAGCGTCAGCGT
GGGCCAGGATGTGCGGTGCCGGCGCCTGGTGCGGGAGGGCACCTACCCCGGAGGCCTGGCT
CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCCACC
ATCTTGTGCACAAATGGTGTGGCCAGGGCCACATAACAGACTGCTGTCTTGGGCTGCCTCAG
GTCCCGAGTAACTTATGTTCAATGTGCCAACACCAGTGGGGAGCCCGCAGGCCTATGTGGCA
GCGTCACCACAGGAGTTGTGGGCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC
AAAGTCTCACCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGCCA
AACCAGACTCGGGTCCCCCTGCTTCCCTTCCCCACTTATCCCCAAGTGCCTTCCCTCAT
GCCTGGGCGCGCCTGACCCGCAATGGGCAGAGGGTGGGTGGGACCCCTGCTGACGGCAGA
GTTCAGGTCCACTGGGCTGAGTGTCCCCTTGGGCCCATGGCCAGTCACTCAGGGGCGAGTT
TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCCTTTTCTAT
TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCTTCTCATGTGAC
AGATGGGGAAACTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCTGCGGGCAGTGGC
ATGACTGGAGCACAGCCTCCTGCCTCCCAGCCCGGACCCAATGCACTTTCTTGTCTCCTCTA
ATAAGCCCCACCCTCCCCGCTGGGCTCCCCTTGCTGCCCTTGCTGTTCCCCATTAGCACA
GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCTCTGACCAGCT
GTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTT
CCAGCCTAGCCAGTTTCTCACCCTGGGTTGGGGTCCCCCAGCATCCAGACTGGAAACCTACC
CATTTTCCCCTGAGCATCCTCTAGATGCTGCCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA
TCTGGCTGGGATCTCCAAGGGGCTCCTGGATTCACTCCCCACTGGCCCTGAGCACGACAGC
CCTTCTTACCCTCCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCCCACCCATGTCTATGC
TCTACCCCCAGGGCAGCATCTCAGCTTCCGAACCTGGGCTGTTTCCTTAGTCTTCATTTTA
TAAAGTTGTTGCCTTTTAAACGGAGTGTCACTTTCAACCGGCCTCCCCTACCCCTGCTGGC
CGGGGATGGAGACATGTCAATTTGTAAAAGCAGAAAAAGGTTGCATTTGTTCACTTTTGTAA
ATTGTCCTGGGCCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC
AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGTCTTCCCCACCTGCCTAGC
CCATCATCTATCTAACCGGTCCTTGATTTAATAAACACTATAAAAGGTTTAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

235/249

FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652

><subunit 1 of 1, 353 aa, 1 stop

><MW: 37847, pI: 6.80, NX(S/T): 2

MPWPLLLLLLAVSGAQTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAAGLGGLTHLSLASLQRLPELAPS
GFRELPGQLQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGG
GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA
AAACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT
GTTCCAGGCCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCAC
GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCC
TCTAGTCTTGCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG
GATTTTCTGAGATACGGGCGAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA
AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT
GCTAAGACTCTATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCC
GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
GCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTC
TGCAATGGATGGAGGAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTTCGAGGT
CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT
GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGAT
TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTGTAAATATCTT
TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTGTCTATTTAATGTATTT
ATTTTTTTTACTTGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG
AGCAGGTGATGTATTTTTTATACAGTAAAAAAAAAAAAACCTTGTAATTCTAGAAGAGTGGCT
AGGGGGGTTATTCATTTGTATTCACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA
TATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATT
GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT
CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA
CCAAAAAAAAAAAAAAAAAAAA

237/249

FIGURE 234

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSEFLTICKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE

Important features of the protein:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

238/249

FIGURE 235

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCG
CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC
CGAGCTAGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG
CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT
TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG
TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATG
GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACCTGACCTAGTGAAGGTTTCAAGATGCAAAT
GGAAGGAAAAAGGAAACTGGAAGGAAAACCATTCGCGATTTTCGTGGTGTACATCATGCATTTG
CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA
AGAGCAGCACTGGTGAATATGGGAGATTTAACCCTTATGATACAGTGAAACACTACTTGGT
ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC
TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA
CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTGAGGCTGT
TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACCATCTTGGCTGAGAATGACCC
CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
TTTTAA

239/249

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568

><subunit 1 of 1, 323 aa, 1 stop

><MW: 36064, pI: 9.33, NX(S/T): 1

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGA
RESAPYRGMVRTALGIIEEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVKSEDEH
YPLWKSVIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFLPSWLRMTFWSMVFWLT
YEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

240/249

FIGURE 237

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC
GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC
TTAAGAAGTAAAAATGGCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG
ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGCAGGTATATTGTTTTTACAGGC
TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT
TCACACATGTGGTGTATTTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTC
AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT
TTCATTGGTTTTCATGTTGATGTTTGGGTCACCTTATTGCTTCCATGTGGATTCTTTTTGGTGC
ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACTTA
TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC
TTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTTGTAGATAGGTTTTTTATCTCTCAGT
ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTTATGTTT
TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTTCATTGCATAGACTGTTAATATGTA
TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATTCCTGAGATTTAGAA
CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT
CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGG
CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT
AAAAATACAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGC
TGAGGCAGGAGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC
TGCACTCTAGCCTGGGGGAGAAAGTGAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC
TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA
TAAAGGTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAATGAGGTTTTTTTGGTAAAGA
AAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCCC
AAAGGACTAGTTTGAAAGCTTCTTTTAAAAGAATTCCTCTAATATGACTTTATGTGAGAA

241/249

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIFGMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFG RTEELWT

Important features:**Signal peptide:**

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

242/249

FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
CTGGCGGGCCCGCAACACTCCGTCTCACCCTCTGGGGCCCACTGCATCTAGAGGAGGGCCGTCT
GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGT
GGTCAGCTGGGTGAGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG
GGAAGTGGGAGCCTCGAGCCCTCGGGTGGGAAGCTGACCCCAAGCCACCCTTCACCTGGACAG
GATGGAGAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA
TGTTTATTGGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
GCCTCGCCACCAAGGAGATCCAGGTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCC
AGCCAACTACTTTGCGTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT
GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCATAACATC
GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG
AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGTGCAGTGGTGCTGGTGG
CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAACTCTTCTCTGACTTG
GGGAGTTCCTACGCAAAACAACTGGGCTTCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA
CCTCAGGGGTAAAAGCCCCCTTTGAGCAGTTCCTTAAAGAACAGCCCAGACACAAACAAATACG
AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTT**TAG**GGTGGC
TGTGGCTCTTCCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCCG
GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGTGCGTGGAAGGTGCTGCAGGTCTTGACGC
TGTGTGCGCCTCTCCTCCTCGGAAACAGAACCCTCCCACAGCACATCCTACCCGGAAGACC
AGCCTCAGAGGGTCCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTTCGTCAGGG
ACTGCTGACGGCTGGTCCTGAGGAAGGACAACTGCCCAGACTTGAGCCCAATTAAATTTTA
TTTTTGCTGGTTTTTGAIAAAAAAAAAAAAAAAAAAAAAA

243/249

FIGURE 240

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

Important features:**Signal peptide:**

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGAT
CCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACA
GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC
TCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCC
CTGCACCCCTTCCCTGGGACACT~~ATG~~TTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCC
TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCA
GCCTCTTACCCTGAGTGTGGAAACAATGCCAGTCGCCCATCGATATTCAGACAGACAGTGT
GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC
CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTG
GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC
CCCAGGGGGGTGAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC
ATTATGACTCTGATTCCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCT
GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
TCACTTGCAATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG
AGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT
TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT
GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA
ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGA
TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG
CCTTCTCCTGGCTGTTTTATTTTCAATGCTAGAAAGATTTCGGAAGAAGAGGCTGGAAAACCGAA
AGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCAT~~TAA~~ATTCCTTCTCAGATACCA
TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG
GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAG
GAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA
GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGG
GAAGTTTGGGATATACCCCAAAGTCCTCTACCCCTCACTTTTATGGCCCTTCCCTAGATA
TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTGTATCAATA
TATTTGGAAATTAAAGTTTCTGACTTT

245/249

FIGURE 242

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPA SYPECGNNAQSPIDIQTDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGGSEHQ
INSEATFAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGT
L FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKS SVVFTSAQATTEA

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 243

AATTTTTCACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTC
GTGGACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTTGTCTTCTAGG
ATCAACTCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACCTGGCTC
CGGATCAGGGAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTG
ATACCATTAACACAGATGCTCACACTGGGGCCAGATCTGCATCTGTAAATCCTGCTGCAGG
AATGACACCTGGTACCCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAAC
TGCACCCACATGTGTTACCAATTTTTGTACACAACCTGGAGCCCAGGGCACTATCCTAAGC
TCAGAGGAATTGCCACAAATCTTCACGAGCCTCATCATCCATTCCCTTGTCCCGGGAGGCAT
CCTGCCCACCAGTCAGGCAGGGGCTAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAG
GAGCAGGTGTAAATCCTGCCACCCAGGGAACCCAGCAGGCCGCCTCCCAACTCCCAGTGGC
ACAGATGACGACTTTGCAGTGACCACCCCTGCAGGCATCCAAAGGAGCACACATGCCATCGA
GGAAGCCACCACAGAATCAGCAAATGGAATTCAGTAAGCTGTTTCAAATTTTTTCAACTAAG
CTGCCTCGAATTTGGTGATACATGTGAATCTTTATCATTGATTATATTATGGAATAGATTGA
GACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATTTACCTGAAAATATTCTTGAAATT
TCAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAACAATAATTCAATGGATAAAT
CTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATATTTAAACATATTTGGAAA
ACTGGAAA
AAAAAAAAAAAAAAAAAAAA

247/249

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGILNVQQQLHPPHVLPIFVTQLGAQGTILSSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTAPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

248/249

FIGURE 245

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCG
GAGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCG
GCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCC
TGCTGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG
CAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
GCCAGCAGGAGTGCCTGGTTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG
GGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTTGAG
GAGTCCTGGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT
TGGGAAAATTGCGGAGTGACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT
TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTTACATTC
AATGGAGCTGAATGTTTCAAGGACCTCTTCCCATTTGAAGCTATAATTTATTTGGACCAAGGAAG
CCCTGAAATGAATTCACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG
GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAA
GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAATA
AATGCTTTAATTTTCATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACTTAAAT
GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA
CCAAAGTGATTTTCACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGT
GGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA
TAATTTGGAATATTGTTGTGGTCTTTTGTCTTTTCTTCTTAGTATAGCATTTTTTAAAAAATA
TAAAAGCTACCAATCTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTAAAT
AAAAATTATTTCCAACA

249/249

FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGGKQKAQLRQREVVDLYNGMCLQGPAGV

PGRDGSPGANVIPGTPGIPGRDGFKEGKECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA

ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGFLPIEAIYLDQGSPEMN

STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

A. CLASSIFICATION OF SUBJECT MATTER IPC 7 C12N15/12 C07K14/47 C07K14/705 C12N15/62 C07K16/18		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) IPC 7 C12N C07K		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practical, search terms used)		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 31799 A (HUMAN GENOME SCIENCES INC ;NI JIAN (US); ROSEN CRAIG A (US); GENTZ) 23 July 1998 (1998-07-23) seq.ID's 6 and 22 page 40 -page 41 page 16, line 3 - line 12 ---	1-27
X	TODD, S.C: ET AL.: "Sequences and expression of six new members of the tetraspandin/TM4SF family." BIOCHIMICA ET BIOPHYSICA ACTA, vol. 1399, 1998, pages 101-4, XP000914781 page 102, left-hand column, paragraph 1; figure 1 --- -/--	1-27
<input checked="" type="checkbox"/> Further documents are listed in the continuation of box C. <input checked="" type="checkbox"/> Patent family members are listed in annex.		
* Special categories of cited documents : "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art. "&" document member of the same patent family		
Date of the actual completion of the international search 21 June 2000		Date of mailing of the international search report 17. 10. 00
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016		Authorized officer Smalt, R

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	MEADA, K. ET AL.: "Cloning and characterization of a novel human gene, TM4SF6, encoding a protein belonging to the transmembrane 4 superfamily, and mapped to Xq22." GENOMICS, vol. 52, 1998, pages 240-2, XP000921144 the whole document ---	1-27
A	EP 0 834 563 A (SMITHKLINE BEECHAM CORP) 8 April 1998 (1998-04-08) the whole document ---	
A	WO 97 07198 A (GENETICS INST) 27 February 1997 (1997-02-27) the whole document ---	
A	YOKOYAMA-KOBAYASHI M ET AL: "A signal sequence detection system using secreted protease activity as an indicator" GENE,NL,ELSEVIER BIOMEDICAL PRESS. AMSTERDAM, vol. 163, no. 2, 3 October 1995 (1995-10-03), pages 193-196, XP004041983 ISSN: 0378-1119 the whole document -----	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 00/04342**Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)**

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Claims 1-27 (all partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: Invention 1: claims 1-27, all partially

Nucleic acid with seq.ID.3, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.4 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.4 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide.

2. Claims: Inventions 2-123: claims 1-27, all partially

As subject 1 but limited to each of the respective protein sequences as in Seq.ID's 6(5), 8(7), 10(9), 17(16), 22(21), 24(23), 29(28), 31(30), 33(32), 41(40), 43(42), 50(49), 52(51), 54(53), 56(55), 58(57), 63(62), 68(67), 70(69), 72(71), 77(76), 79(78), 84(83), 86(85), 88(87), 95(94), 100(99), 102(101), 104(103), 111(110), 116(115), 118(117), 123(122), 128(127), 130(129), 132(131), 134(133), 136(135), 138(137), 140(139), 142(141), 144(143), 146(145), 148(147), 153(152), 158(157), 160(159), 162(161), 170(169), 180(179), 189(188), 194(193), 196(195), 198(197), 203(202), 210(209), 212(211), 214(213), 216(215), 218(217), 220(219), 225(224), 227(226), 229(228), 234(233), 236(235), 243(242), 248(247), 253(252), 260(259), 265(264), 267(266), 269(268), 271(270), 273(272), 275(274), 277(276), 282(281), 287(286), 292(291), 297(296), 302(301), 304(303), 306(305), 308(307), 310(309), 315(314), 317(316), 322(321), 324(323), 326(325), 328(327), 330(329), 332(331), 334(333), 336(335), 338(337), 340(339), 347(346), 352(351), 354(353), 356(355), 358(357), 364(363), 366(365), 372(371), 374(373), 376(375), 378(377), 383(382), 385(384), 390(389), 395(394), 397(396), 402(401), 406(405), 410(409), 415(414), 423(422), 429(428), and 431(430) (corresponding nucleic acid sequences indicated between brackets).

For the sake of conciseness, the first subject matter is explicitly defined, the other subject matters are defined by analogy thereto.

INTERNATIONAL SEARCH REPORT

International Application No

P-~~US~~ 00/04342

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9831799 A	23-07-1998	AU 5923398 A	07-08-1998
		AU 6030398 A	07-08-1998
		EP 0972022 A	19-01-2000
		EP 1007663 A	14-06-2000
		WO 9831800 A	23-07-1998
		AU 5927398 A	07-08-1998
		AU 6241698 A	07-08-1998
		EP 0972023 A	19-01-2000
		EP 0972025 A	19-01-2000
		EP 0988385 A	29-03-2000
		WO 9831818 A	23-07-1998
		WO 9831801 A	23-07-1998
		WO 9831806 A	23-07-1998
EP 0834563 A	08-04-1998	JP 10179178 A	07-07-1998
		US 5824504 A	20-10-1998
WO 9707198 A	27-02-1997	US 5707829 A	13-01-1998
		AU 6712396 A	18-02-1997
		AU 6768596 A	12-03-1997
		CA 2227220 A	06-02-1997
		CA 2229208 A	27-02-1997
		EP 0839196 A	06-05-1998
		EP 0851875 A	08-07-1998
		JP 11510045 T	07-09-1999
		US 6043344 A	28-03-2000
		WO 9704097 A	06-02-1997
		US 6074849 A	13-06-2000
		US 5969093 A	19-10-1999